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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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19.
19.
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Gapop 10.0 , Gapext 1.0
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100.0
56.5
56.5
56.5
55.9
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                                                                                                                                                                                                                                       Query
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
                                                                                                                                                                                                                 Length
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/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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                                                          AAF72234
AAH68525
ABL89671
                      AAS41599
AAS29698
                                                                                                                              AAH65584
AAH65585
                                                                                                                                                                           AAA96849
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                                                                            Guide desoxynucleo
C glutamicum codin
C glutamicum codin
C glutamicum gl
Corynebacterium gl
C glutamicum codin
                                                                                                                                                                                                               Description
             Human polynucleoti
cDNA encoding nove
Human endocrine po
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Human G-protein-co	ABK30419	24	507.	51.8	17.6	45	
	AAF22305	21	1082138	52.4	17.8	44	a
Human cDNA sequenc	AAS21261	22	3371	52.4	17.8	43	a
Human immune/haema	AAK85124	22	1804	52.4	17.8	42	
Human immune/haema	AAK77850	22	1804	52.4	17.8	41	
Genomic sequence #	AAS09226	22	1804	52.4	17.8	40	a
DNA encoding novel	AAS65336	23	371	52.4	17.8	39	
Human neuregulin-1	AAK96733	22	1503900	52.9	. 18	38	a
Human neuregulin-1	AAK95240	22	1503900	52.9	18	37	a
Complete genome se		20	N	52.9	18	36	
Drosophila melanog	ABL04292	23	13437	52.9	18	35	
Drosophila melanog	ABL04293	23		52.9	18	3 4	C
Rat neuronal immed	AAZ28289	20		52.9	18	33	
Murine chemokine c	AAA74870	21		52.9	18	32	a
Human prostate exp		23		52.9	18	31	a
Rhizobium species		19		53.5	18.2	30	a
Rhizobium species		19		53.5	18.2	29	a
Drosophila melanog	ABL16586	23		53.5	18.2	28	
Human nervous syst		22		53.5	18.2	27	a
Vector containing		14		53.5	18.2	26	
ACV synthetase gen		12		53.5	18.2	25	
Early onset Alzhei	AAT59476	18		53.5	18.2	24	
Listeria innocua D		24		54.1	18.4	23	a
Listeria innocua c		24	1163020	54.1	18.4	22	a
Leukaemia-associat		24		54.1	18.4	21	
Leukaemia-associat		24		54.1	18.4	20	
Leukaemia-associat		24		54.1	18.4	19	C
DNA encoding novel		23		54.1	18.4	18	a
DNA encoding novel	AAS88724	23		54.1	18.4	17	C
DNA encoding novel	AAS86004	23		54.1	18.4	16	
C. albicans essent	AAS23463	22	86	54.1	18.4	15	a
opsis t	AAF22303	21	611590	54.7	18.6	14	
Human immune syste	ABL33550	24	6075	54.7	•	13	O
Aspergillus oryzae	AAD04180	22	1884		18.8	12	
Aspergillus oryzae	AAF13367	21	1015	55.3	18.8	11	
cDNA encoding nove	AAS41061	22	3489	55.9	19	10	a

a O a

ALIGNMENTS

RESULT 1 AAA96849

AAA96849 standard; DNA; 34 BP

Guide desoxynucleotide building block G1

19-FEB-2001 AAA96849;

(first entry)

0.0

0.0

Rance I, Gruber V, Theisen M;	(MERI-) MERISTEM THERAPEUTICS.	29-MAR-1999; 99FR-0003925.	29-MAR-2000; 2000WO-IB00370.	05-OCT-2000.	WO200058485-A1.	Synthetic.	Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; ss.

2874

endocrine

Chimeric expression promoter for transgenic plant production, comprises

WPI; 2000-647238/62

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RESULT 2
AAH65584
ID AAH6
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Best Local
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07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                              Nakagawa
Tateishi
                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence from with sequence
                                                                                                                                    WPI; 2001-376931/40.
P-PSDB; AAG90365.
                                                                                                                                                                                                                                                                                                      18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                        EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH65584 standard; DNA; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                      Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                  20-JUN-2001
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                                                                                                                                                                             z œ
                                    SEQ ID NO: 619; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                               ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 8 A; 9 C; 7 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                           Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
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                                                                                                                                                                                                                                                                                                                                                                                                                               acid synthesis; vitamin; saccharide;
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Pred. No. 3.5e-06;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum.

These

mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

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RESULT 3
AAH65585/c
ID AAH655
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are useful for identifying the mutation point of a gene derived from a mutant of corymeform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Corymeform bacterium, and identifying a homologue of a gene derived from corymeform bacterium. Corymeform bacteria are useful for producing amino acide, nucleic acide, vitamins, saccharides and organic acide, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                          WPI; 2001-376931/40.
P-PSDB; AAG90366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not specification, but was obtained in electronic fo
                                                                                                           The present invention provides a number of nucleotide and protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Patent
                                                                                                                                   Claim 8; SEQ ID NO: 620;
                                                                                                                                                                                                                                                                                                 (КУОМ ) КУОМА НАККО КОСУО
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis; ds
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75.0%;
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Ikeda M, Ozaki A;
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Best Local S
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                                                                                                                                                                                                                                                                                                              25-JUN-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum; metabolic pathway protein; fine chemical production; microorganism; organic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF72234 standard; DNA; 666 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 612 BP; 147 A; 159 C; 171 G; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                          23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                             04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                              nonproteinogenic
lipid; saturated
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                                                                                                                                          3-JUL-1999;
3-JUL-1999;
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                  -JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                   teinogenic amino acid; purine base; pyrimidine base; nucleotide; saturated fatty acid; unsaturated fatty acid; diol; vitamin; ydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
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                                                                                                                                                                                                                                                                                                                                          2000WO-IB00923.
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                          99DE-1031478
99DE-1031510
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99DE-1031632
99DE-1031634
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99DE-1032126
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99DE-1031465
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99DE-1031415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutamicum MP protein nucleotide sequence SEQ ID NO:963.
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Pred. No. 39;
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RESULT 5
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14-JUL-1999;
14-JUL-1999;
14-JUL-1999;
14-JUL-1999;
12-AUG-1999;
27-AUG-1999;
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31-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino and purine and pyrimidine bases -
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03-SEP-1999;
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03-SEP-1999;
                                                                                                                                     C glutamicum
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03-SEP-1999;
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27-AUG-1999;
                   Corynebacterium glutamicum
                                                                organic
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                                                                  acid synthesis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vitamins, cofactors, polyketides and enzymes.
                                                                                     bacterium; amino
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                                                                                                                                     coding sequence fragment
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99DE-1042086.
99DE-1042087.
99DE-1042088.
99DE-1042129.
99DE-1042124.
99DE-1042129.
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75.0%;
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                                                                                        acid
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Pred. No. 40;
0; Mismatches
                                                                                        synthesis; vitamin; saccharide;
                                                                                                                                   SEQ ID NO: 7060
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RESULT 6
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XX LIVER ABL896
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XX CYLOST
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XX HOMO 8
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XX PP WO2001
XX PD 29-NOV
XX YF 18-MA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                     vulnerary; anticonvulsant; cardiant; gene therapy; car neurological disease; infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identif mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                             18-MAY-2001; 2001WO-US16450
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 233.
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                                                                                    29-NOV-2001.
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24; Conservative
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                                                                                                                                                                                                                                                                            immunosuppressive; nootropic; c; hepatotropic; antidabetic; antibacterial; anticonvulsant; antibacterial; ene therapy; cancer; immune dis
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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da M, Oz
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Ozaki A;
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1.1e+02;
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sorder; cardiovascular disc
                                                                                                                                                                                                                                                                                                                                   neuroprotective; antiviral; antiinflammatory; antiulcer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for identifying
e, analysing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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The invention relates to novel genes (ABL89449-ABL90853) and proteins CC (ABB99040-ABB99444) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the genes are CC me nucleic acids, proteins, antibodies and (ant)agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's Cdisease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC note: The sequence data for this
RESULT 7
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Matches
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                                                                                                                                                                                            Human; oxidoreductase enzyme; transferase; nydrorase, received ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; reardiovascular disorder; reproductive disorder; reproductive disorder; reproductive disorder; gene therapy; cyto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 1405 isolated polypeptides, useful for diagnosis, treatment prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferati
                                                                                                                                                                                                                                                                                                  cDNA encoding novel human enzyme polypeptide #815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                             17-JAN-2001; 2001WO-US01239
                                                                                                                                                                                  anti arthritic;
                                                                                                                                                                                                                                                                                                                                   17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                    AAS41599;
                                                                                                                                                                                                                                                                                                                                                                                                      AAS41599 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 447 BP; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
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                                                                                                               WO200155301-A2
                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACTCCTCTACTTATCGATCGGTACTG
                                                                                                                                               sapiens
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llarity 81.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                nephrotropic;
                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                  anticoagulant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 T; 1 other;
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                                                                                                                                                                                                                                                                    isomerase;
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31-JAN-2000; 2000US-0179065 04-FEB-2000; 2000US-0180628

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02-OCT-2000
13-OCT-2000
20-OCT-2000
20-NOV-2000
20-OCT-2000
20-NOV-2000
20-DEC-2000
20-DEC
Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cance diseases
                                                                         WPI; 2001-465566/50.
P-PSDB; AAU23729.
                                                                                                                     Rosen
                                                                                                                                                   (HUMA-)
                                                                                                                  ÇĄ
                                                                                                                                                   HUMAN
                                                                                                                    Barash
                                                                                                                                                                             2000US-0237039
2000US-0237039
2000US-0239337
2000US-02319357
2000US-0241786
2000US-02411809
2000US-0241809
2000US-02446176
2000US-0246476
2000US-0246477
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2000US-0246523
2000US-0246523
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0246611
2000US-0249211
2000US-02511861
2000US-02511868
2000US-02511868
2000US-02511868
2000US-02511898
2000US-0251989
                                                                                                                                                   GENOME
                                                                                                                     SC,
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                                                                                                                     Ruben
                                                                                                                                                   INC
                                                                                                                     NS.
              cancerous
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16-MAR-2000
11-MAR-2000
11-MAR-2000
11-MAR-2000
20-JUN-2000
20-JUN-2000
20-JUN-2000
21-JUN-2000
11-JUL-2000
11-JUL

2000US-018464.
2000US-019976.
2000US-019976.
2000US-019976.
2000US-0209467.
2000US-0211486.
2000US-0211486.
2000US-0211486.
2000US-0211486.
2000US-0211496.
2000US-0211496.
2000US-0212491.
2000US-021251.
2000US-022521.
2000US-022521.
2000US-0225267.
2000US-0225268.
2000US-022528.
2000US-022528.
2000US-022528.
2000US-022528.
2000US-022528.
2000US-0235447.
2000US-0235447.
2000US-0235447.
2000US-0235447.
2000US-0235447.
2000US-0235447.
2000US-023548.
2000US-0233163.
2000US-0233163.
2000US-0233499.
2000US-0235834.
2000US-0235838.

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RESULT 8

AAS29698/C

AAS296

XX

AAS296

XX

AAS296

XX

AAS296

XX

ACCEPTON

XX

CAT; d

XW

CAT; d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel human enzyme cc polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences cc encoding them. The enzyme polypeptides of the invention may comprise the cf functional classes of exidoreductases, transferases, hydrolases, lyasses, it can be remarked to a control of the invention are useful in the cd disgnosis, treatment, prevention and/or prognosis of a wide range of cd disorders including hyperproliferative disorders (e.g. cancer), cc immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cancer), cc (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), cc (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. anthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. arthritis) and infectious disorders (e.g. atherosclerosis), cc (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), cc (e.g. infertility) and infectious disorders (e.g. inflammatory disorders (e.g. infertility) and infectious disorders (e.g. inflammatory disorders (e.g. infertility) and infectious disorders (e.g. inflammatory disorders (e.g. infertility) and infectious disorders (e.g. infertility). The sequence of the invention can also be used in gene therapy. cc AAS40785-AAS41894 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.

Cc Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figure and specification, but was obtained in electronic format directly from WIPO at figure and specification.
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Best Local S
Matches 22
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastroiptestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility.
                                                                                                                                                                                                                                  17-JAN-2001;
                                                                                                                                                                                                                                                                             02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human endocrine polypeptide encoding cDNA SEQ ID No 198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0190076.
2000US-0205515.
2000US-0205467.
                                                                                                                                                                                                                                  2001WO-US01308
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                                                                                                                                                                                       200005-0179065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB:
Pred. No. 48;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T, 5
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    14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
12-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
01-SEP
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11-JUL-2000
14-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
2000US-0214886

2000US-02116497

2000US-02116497

2000US-0217496

2000US-0217496

2000US-02245118

2000US-0225513

2000US-0225211

2000US-0225266

2000US-0225275

2000US-0225276

2000US-02252775

2000US-0225477

2000US-0225447

2000US-0231413

2000US-0231414

2000US-0231414

2000US-0231414

2000US-0231414

2000US-0231499

2000US-0231499

2000US-0231499

2000US-02315834

2000US-02315834

2000US-02315834

2000US-02315834

2000US-02317039

2000US-02319937

2000US-02319937
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08-NOV-2000
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01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the endocrine polypeptides of the invention. Endocrine polypeptides and thei associated polynucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnos
                                                            Claim
                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
                                                                                                                      P-PSDB;
                                                                                                                                                                        (HUMA-)
                                                                                                                                2001-451936/48.
                                                          ٠,
                                                                                                                                                                        HUMAN
                                                                                                                      AAU18469.
                                                                                                                                                  Barash SC,
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2000US-0246613.
2000US-0249207.
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2000US-0246526.
2000US-0246527.
2000US-0246528.
2000US-0246528.
2000US-0246532.
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2000US-0246475.

2000US-0246476.

2000US-0246477.

2000US-0246477.

2000US-0246478.
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2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0249245.
2000US-0249264.
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2000US-0249216.
2000US-0249217.
2000US-0249217.
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2000US-0251869.
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2000US-0249211.
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2000US-0249209.
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2000US-0244617.
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                                                                                                                                                                                                              2000US-0251990.
                                                                                                                                                                        GENOME
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                                                          198;
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                                                                                                                                                                        SCI INC.
                                                                                                                                                   Ruben
                                                          604pp; English
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8888888888888888888888
S
                                                                                                                                                                                                                                                      CC pathological condition can be determined by determining the presence or cabsence of a mutation in an endocrine polynucleotide. The treatable cdisorders include autoimmune diseases such as rheumatoid arthritis, chyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular cdisorders such as cardiac arrest, cerebrovascular cdisorders such as cardiac arrest, cerebrovascular cdisorders such as corneal infection, nervous system disorders such as cardiac arrest, cerebrovascular coular disorders such as corneal infection, endocrine disorders such as corneature labour and infertility, gastrointestinal disorders such as corneature labour and infertility, gastrointestinal disorders such as corneature labour and infertility, gastrointestinal disorders such as corneature labour and infertility as a sthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain corgans before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to correase or decrease storage capabilities.

Conceints the sequence data for this patent did not form part of the printed cornection by the cornection of the printed cornection of the p
                                                                                    Matches
                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                               specification,
       1 GACTCCTCTACTTATCGATCGGTACTG
                                                                                                               Similarity
                                                                                    Conservative
                                                                                                                                                                                                                                  but was obtained in
                                                                                                               55.9%;
81.5%;
                                                                                0;
                                                                                Score 19; DB Pred. No. 48; 0; Mismatches
       27
                                                                                                                                                                                                                               electronic
                                                                                                                                                      22;
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                                                                                                                                                                                                                                  format
                                                                                                                                                      Length 521;
                                                                                    Indels
                                                                                                                                                                                                                           directly
                                                                                0;
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                                                                                Gaps
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RESULT 9
AAS29578/c
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                                                                 AAS29578
  Human
                                             AAS29578;
                       21-NOV-2001
                                                                                                                     198 GACTGCGCTGCTTATGCATCGGTACTG
  endocrine
                                                                 standard; cDNA;
                      (first entry)
polypeptide encoding cDNA SEQ
                                                                  2874
                                                                  ΒP
                                                                                                                       172
  ID No
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Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer, ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; brasst; liver; cardiovascular disorder; se; cerebrovascular disorder; prevous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility.

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104-PEB-2000;
24-FEB-2000;
22-FEB-2000;
16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
19-MAY-2000;
29-UN-2000;
28-UN-2000;
30-UN-2000;
30-UN-2000;
30-UN-2000;
11-UTL-2000;
11-UTL-2000;
11-UTL-2000;
11-UTL-2000;
                                                                                                      31-JAN-2000;
                                                                                                                                 02-AUG-2001.
                                                                                                                     17-JAN-2001;
                                                                                                                                                WO200155364-A2
                                                                                                                                                              Homo
                                                                                                                                                             sapiens.
2000US-0179065

2000US-0180628

2000US-0184664

2000US-0189374

2000US-0199174

2000US-0199123

2000US-0205515

2000US-0205467

2000US-0214886

2000US-0216487

2000US-0216488

2000US-0216488

2000US-0217487

2000US-0217487

2000US-0217487

2000US-0217487

2000US-0217487
                                                                                                                     2001WO-US01308
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diagnosis

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26-JUL-2000 26-JUL-2000 14-AUG-2000 14-AUG-2000

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08-NOV-2000
17-NOV-2000
17-NOV
Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the endocrine polypeptides of the invention. Endocrine polypeptides and their associated polymucleotides of the invention are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polymucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular alsonders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular and fungi, alzheimer's disease, infections caused by bacteria, viruses and fungi,
                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders of the endocrine system such as reproductive disorders, endocrine cancers and also for testing and detection e.g. diagnosis
                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
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DB; AAU18349.
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2000US-0246477.
2000US-0246523.
2000US-0246528.
2000US-0246528.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0249207.
2000US-0249207.
2000US-0249211.
2000US-024921.
2000US-024921.
2000US-024921.
2000US-024921.
2000US-024921.
2000US-024921.
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                                                                                                                                                                                                                                                                                                                                                       604pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
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2000US-0230438 2000US-0231243 2000US-0231244 2000US-0231244 2000US-0231413 2000US-0231413 2000US-0232080 2000US-0232081 2000US-0232081 2000US-023297 2000US-023297 2000US-023298 2000US-023298 2000US-023299 2000US-0232401

2000US-0226868 2000US-0227182 2000US-022709 2000US-0229287 2000US-0229287 2000US-0229343 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229509 2000US-0229509 2000US-0229509 2000US-0225758. 2000US-0225759. 2000US-0226279.

114-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
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27-SEP-2000
28-SEP-2000
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2000US-0233063 2000US-0233064 2000US-0234274 2000US-023499 2000US-02354844 2000US-02354844 2000US-0235836 2000US-0235836 2000US-0236367 2000US-0236367 2000US-023637 2000US-023687 2000US-023687 2000US-023687 2000US-023687 2000US-023687 2000US-023687 2000US-023687 2000US-023687 2000US-023697 2000US-023697 2000US-0237039 2000US-0237039 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241809 2000US-0244817

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RESULT 10
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Matches 22
 19-MAY-2000
07-UUN-2000
28-UUN-2000
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11-JUL-2000
11-JUL-2000
11-JUL-2000
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26-JUL-2000
14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
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6-MAR-2000;
7-MAR-2000;
8-APR-2000;
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22; Conservative
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                                                                         2000US-0220963.

2000US-0229544.

2000US-0224518.

2000US-0224519.

2000US-0225213.

2000US-0225214.

2000US-0225266.
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2000US-0184664

2000US-0186350

2000US-0190076

2000US-0190123

2000US-0198123

2000US-0205515

2000US-020467

2000US-0214886

2000US-0214886

2000US-0216647

2000US-0216847

2000US-0216847
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2000US-0218290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious disorder; gene ropic; anticoagulant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB Pred. No. 62; 0; Mismatches
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02-OCT-2000
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2000US-0225758
2000US-0225759
2000US-0226681
2000US-0226881
2000US-0229343
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2000US-02330437
2000US-0231244
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2000US-0246528
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81.5%;

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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lysses, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders
                         Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                      metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynuclectides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-465566/50.
P-PSDB; AAU23191.
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                                                                                                                                                                                                                                                                                                                                                                      diseases
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format
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Query Match

Sequence 3489

BP;

835 A; 859

ü Score 960 19; ູດ

832 T; 3 멂 .22

of the printed

Length 3489; other;

Sequence 1015 BP;

233 A;

280 C;

259 G; 243 T; 0 other,

55.9%;

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RESULT 11
AAF13367
CC expression of genes in a first filamentous fungal (FF) cell relative to ceapression of the same genes in one or more second filamentous fungal (CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC discovered, possible functions of unknown open reading frames can be CC discovered, possible functions of unknown open reading frames can be CC discovered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC morphogenesis, recombination, metabolic or catabolic pathway compineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an CC array equals one gene or open reading frame, and organisation of the CC microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11237 represents ESTs from Aspergillus CC ricar. AEF11647 represents ESTs from Aspergillus and COVIDER and COVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus organ; Trichoderma resen; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF13367 standard; cDNA; 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2000; 2000WO-US07781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multiple gene expression; filamentous fungal cell; EST;
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                                                                niger; AAF11854 to AAF14878 represents ESTs from Aspergillus (
AAF14879 to AAF15337 represents ESTs from Trichoderma reesei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for monitoring differential
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NOVO NORDISK AS.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                   The present sequence is a DNA encoding Aspergillus oryzae lysophospholipase-1 (LLPL-1). Lysophospholipase is an enzyme that hydrolyses lysophospholipids into fatty acids. The DNA encoding LLPL-1 is cloned into a plasmid present in Escherichia coli deposit number DSM 13082. Lysophospholipase is used to hydrolyse fatty acyl groups in a phospholipid or lysophospholipid and for improving filterability of an aqueous solution or slurry of carbohydrate origin which contains phospholipid and preferably a starch hydrolysate, particularly wheat starch hydrolysate. Lysophospholipase is also used to release fatty acids from intact phospholipid e.g. lecithin, and in the preparation of bakery products such as dough, bread, and cakes to improve elasticity. Lysophospholipase is used to reduce the phospholipid content in an edible bil e.g. vegetable oils such as rape seed oil, soybean oil and
                                                                                                                                                                                                                                                  New lysophospholipase enzyme useful in hydrolyzing fatty acyl groups a phospholipid or lysophospholipid, and in improving filterability of an aqueous solution or slurry of carbohydrate origin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysophospholipase; LLPL-1; lysophospholipid; lecithin; bakery product; dough; bread; cake; elasticity; edible soybean; sunflower; ds.
                                                                                                                                                                                                                         Claim 4; Page 39-42;
                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                     WPI; 2001-282018/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2000; 2000WO-DK00577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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64..1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
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                                                                                                                                                                                                                         58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Aspergillus oryzae LLPL-1 protein"
                                                                                                                                                                                                                                                                                                                                             Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; I
Pred. No. 65;
0; Mismatches
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oil; rape seed;
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Sequence 1884 BP; 429

A; 556 C;

463

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436 T; 0 other;

RESULT 14

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RESULT 13
ABL33550/c
ID ABL335
AC ABL35
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                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                  including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                 genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                    Sequence 6075 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine
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                                             2 ACTCCTCTACTTATCGATCGGTACTGTGAGACA 34
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ACACCTCTACTTATCAACCGAAACAACGAAACA
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                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                  invention provides a number of human immune system associated
                                                                                                   Conservative
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                                                                                                                                                                                                    1318 A; 146 C; 1645 G; 2966 T;
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment of chemically modified gene, us
ment of diseases associated with abnormal
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Pred. No. 72;
0; Mismatches
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                                                                                                   Pred. No. 1.10
0; Mismatches
                                                                                                                            Score 18.6;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German.
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                                                                                                                                                 Length 6075;
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RESULT 15
AAS23463/c
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Best Local Similarity
Thes 24; Conserve
Db 384616 GAGACATCTACTTAGTTATCGGTACTCGGACAC 384648
                                                        Gene identification; essential gene; GRACE; pathogenic fungus; gene replacement and conditional expression; fungal infection; PCR primer; KO-Up; ss.
                                                                                                         C. albicans essential gene knockout upstream PCR primer
                                                                                                                                   04-DEC-2001
                                                                                                                                                                                    AAS23463 standard; DNA; 86
                                                                                                                                                                                                                                                                                                                                                                                           (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing approach to the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                               Sequence 611590 BP; 181893 A; 124460 C; 120254 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 45; Page 820-959; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-587529/55.
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18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                  Candida albicans
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17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      elected
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                              1 GACTCCTCTACTTATCGATCGGTACTGTGAGAC 33
                                                                                                                                                                                                                                                                                                                                                                        proteins such as hormones, cytokines, antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      michrosome; vector; ds.
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                                                                                                                                   (first entry)
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99US-0134770.
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72.7%;
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                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                           Score 18.6; DB 21;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                           (KO-Up)
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Query Match
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Matches 22
                                                                                                                                                                            strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus funigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAS23403 represent C. albicans essential gene knockout upstream PCR primers (KO-Up) used in the methods of the
                                                                                                                                            Sequence 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 255; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roemer T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2000; 2000US-0183534.
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4 TCCTCTACTTATCGATCGGTACTGTGAG 31
                                                 l Similarity
22; Conserv
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                                                   Conservative
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78.6%;
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                                       Pred. No. 60;
0; Mismatches
                                                                          Score 18.4;
Pred. No. 6
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                                                                                                                                               0 other;
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Result
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Maximum DB seq length: 200000000
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                18
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1
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/cgn2 6/ptodata/1/ina/6A COMB.seq:*
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US-08-222-617A-24

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US-09-280-116-189

US-09-280-116-191

US-08-974-022-1

US-08-795-445A-1

US-08-795-447A-1

US-08-795-446B-1

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US-08-795-446B-1

US-08-795-46B-1

US-08-795-46B-1

US-08-795-516B-2

US-08-361-081-2

US-08-361-081-2

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US-08-361-081-2

US-08-361-558-2
                            US-08-375-235-1

US-07-755-009-1

US-07-755-009-2

US-08-331-644-3

PCT-US93-04102-3

US-09-303-664-40

US-09-086-503-40
US-09-134-001C-1324
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Sequence 2, Appli
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Sequence 24, Appli
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                   3, Appli
40, Appl
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48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	49.4	49.4	49.4	50.0
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Sequence 155, App	Sequence 12, Appl	Sequence 15, Appl	Sequence 155, App	Sequence 12, Appl	Sequence 155, App	Sequence 12, Appl		-	Sequence 50, Appl	-	-	Sequence 50, Appl	Sequence 50, Appl	Sequence 844, App	Sequence 7, Appli	Seguence 1, Appli	Sequence 70, Appl

ALIGNMENTS

RESULT 1 US-09-026-033-1/c

Sequence 1, Application US/09026033 Patent No. 6368791

GENERAL INFORMATION:
APPLICANT: Felix, Carc
APPLICANT: Jones, Doug
APPLICANT: Rappaport,

Felix, Carolyn A. Jones, Douglas H.

NUMBER OF COUNTRY OF THE PROPERTY OF THE PROPERTY OF CORRESPONDENCE ADDRESS: PANTICH SCHWARZE JACOBS & NADEL, P.C.
ADDRESSEE: PANTICH SCHWARZE JACOBS & NADEL, P.C.
ADDRESSEE: One Commerce Square, 2005 Market Street, 22nd

Philadelphia

NUMBER OF SEQUENCES:

TITLE OF INVENTION: METHOD AND KITS FOR ANALYSIS TITLE OF INVENTION: CHROMOSOMAL REARRANGEMENTS AS

ASSOCIATED WITH LEUKEMIA

Eric

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COUNTRY: U.S.A.

ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,033
FILING DATE: 19-FEB-1998
CLASSIFICATION UNMEER: US 60/038,624
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/038,624
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/056,923
FILING DATE: 26-AUG-1997
PRIOR APPLICATION NUMBER: US 60/056,921
APPLICATION NUMBER: US 60/056,921
PRIOR APPLICATION NUMBER: US 60/065,911
APPLICATION NUMBER: US 60/065,911
APPLICATION NUMBER: US 60/065,911
                  TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pair
TYPE: nucleic acid
                                                                                                                                                  REFERENCE/DOCKET NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600-10U1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1294
TELEFAX. 215-965-1294
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60, FILING DATE: 17-NOV-1997
ATTORNEY/AGENT INFORMATION: NAME: DOYLE LEATY, Ph.D., REGISTRATION NUMBER: 36,3:
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STRANDEDNESS:
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ucleic acid
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Query Match
Best Local Similarity
Matches 22; Conserve
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APPLICANT: Fellx, Carolyn A.
APPLICANT: Jones, Douglas H.
APPLICANT: Rappaport, Eric
APPLICANT: Rappaport, Eric
TITLE OF INVENTION: METHOD AND KITS FOR ANALYSIS OF
TITLE OF INVENTION: CHROMOSOMAL REARRANGEMENTS ASSOCIATED WITH LEUKEMIA
                                                                                                                                                                                                      TELEX: 831-494
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELEPHONE: 215-965-1284
TELEPAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/065,911 FILING DATE: 17-NOV-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AUG-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 19-FEB-19
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 60/038,624
                                                                                                                                                                                                                          TELEFAX: 831-494
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STREET: Floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                     NAME: Doyle Leary, Ph.D., REGISTRATION NUMBER: 36,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 26-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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7 TCTACTTATCGATCGGTACTGTGAGACA 34
                                                                                                                                                                                          ENGTH:
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One Commerce Square, 2005 Market Street, 22nd
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78.6%;
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                                                               Score 18.4;
Pred. No. 11;
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Pred. No. 11
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US-09-026-033-3
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                                                                                                                                          Matches
                                                                                                                                                                         Query Match
                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60.
FILING DATE: 26-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60.
FILING DATE: 17-NOV-1997
                                                                     6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: One Commerce Square, 2005 Market Street, 22nd
                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 60/038,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2544 TTTACTTATTGATTGGCACTGTGGGCCA 2571
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD AND KITS FOR ANALYSIS OF THE WITH LEUKEMIA TITLE OF INVENTION: CHROMOSOMAL REARRANGEMENTS ASSOCIATED WITH LEUKEMIA
                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215-965-12
TELEFAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Doyle Leary, Ph.D., Kare REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION: M
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                      7 TCTACTTATCGATCGGTACTGTGAGACA 34
                                                                                                                                                                                                                                                                                                LENGTH: 6987 base pairs
                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: U.S.A.
19103-7086
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1997
                                                                                                                                                                                                                            DNA (genomic)
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                                                                                                                                                         54.1%;
78.6%;
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                                                                                                                                                         Score 18.4;
Pred. No. 1
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                                                                                                                                            Mismatches
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Sequence 23, Application US/09026033 Patent No. 6368791

GENERAL INFORMATION:
APPLICANT: Felix,
APPLICANT: Jones,

Carolyn A. Douglas H.

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                                                                                                                                                                                                                                                    US-08-222-617A-3
                                                                                                                                                                                                            Sequence 3, App...
Sequence 3, App...
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                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    6196 TTTACTTATTGATTGGCACTGTGGGCCA 6223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 6990 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/038,624 FILING DATE: 19-FEB-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rappaport, Eric TITLE OF INVENTION: METHOD TITLE OF INVENTION: CHROMOS NUMBER OF SEQUENCES: 23
                   TITLE OF INVENTION:
                                                   APPLICANT:
                                                                                                    APPLICANT:
                                                                                                                    APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                   APPLICANT:
                                                                                    APPLICANT:
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 26-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
PILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
   INVENTION:
                                                                                                                                                                                                                                    Application US/08222617A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6990 base pairs
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Van Liempt, Henk
Montenegro, Eduardo P.
WENTION: A Method for Influencing Beta-Lactam
VENTION: Antibiotic Production and for Isolation
VENTION: Quantities of ACV Synthetase
                                                                                 Von Doehren, Hans
Palissa, Harriet
                                                                                                                  Gutierrez, Santiago
Barredo, Jose L.
                                                                                                                                                 Martin, Juan F. Garcia, Bruno D.
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26-AUG-1997
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Pred. No. 13;
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RESULT 6
US-08-222-617A-24
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
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NAME/KEY: CDS
LOCATION: 388..11526
OTHER INFORMATION: /fi
OTHER INFORMATION: /pi
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                    CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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                                                                  NUMBER OF SEQUENCES:
                                                                                            TITLE OF INVENTION:
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                                                                                 TITLE OF INVENTION:
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LOCATION:
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OTHER INFORMATION:
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                         STREET:
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Chicago
Illinois
                                                                                                            INVENTION:
                                                                                                                                                                                                                                                                       Application US/08222617A
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                        E: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                  Gartierrez, Santago L.
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300 South Wacker Drive
                                                                                         Van Liempt, Henk

Montenegro, Eduardo P.

WENTION: A Method for Influencing Beta-Lactam

VENTION: Antibiotic Production and for Isolati
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Palissa, Harriet
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87.0%;
                                                                  Quantities of ACV Synthetase 27
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/product= "ACV Synthetase"
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Xaa=Ala or Ser ".
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Pred. No. 19;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati

Version #1

COUNTRY:

60606

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APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT FILING DATE: 1990-03-26
CURRENT FILING DATE: 1990-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 189
LENGTH: 507
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 189, Application US/09280116A Patent No. 6331427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                           Query Match
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                                                                                                        -09-280-116-189
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INFORMATION FOR SEQ ID NO: 24:
                                                                                                              PEATURE: misc_feature LOCATION: (1) _ (507)
OTHER INFORMATION: n = a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11163 ACTTATCGATCCGTACTTTGACA 11185
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                     FEATURE:
OTHER INFORMATION: asticin/m 12a metalloproteases
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ATTORNEY/AGENT INFORMATION:
97,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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OTHER INFORMATION:
OTHER INFORMATION:
                                            Local Similarity 83.3 to 20; Conservative
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LOCATION:
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CTCTACTTATCGATCGGTACTGTG
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INFORMATION: /product= "ACV Synthetase"
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04-APR-1994
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                                                           51.8%;
83.3%;
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                                              <u>.</u>
                                                           Score 17.6;
Pred. No. 18;
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Pred. No. 19;
                  29
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                                              Mismatches
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                                                                         Length 507;
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/175965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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Best Local Similarity
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              ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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LOCATION: (1)...(933)
OTHER INFORMATION: n = a,
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TYPE: DNA
ORGANISM: Homo sapiens
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                STREET: 1890 CITY: Thousand Oaks
STATE: California
                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CTCCTCTTATAGATCGTTACTGTG 312
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                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             COUNTRY:
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2432 base pairs
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83.3%;
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                                                                                                                        08/577,788
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Pred. No. 20
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RESULT 11
US-08-795-447A-1
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US-08-974-022-1
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; LOCATION:
US-08-795-445A-1
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Patent No. 6
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Best Local Similarity 77.8
Matches 21; Conservative
                                                                                                                         Matches
                                                                                                                                      Query Match
Best Local Similarity
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
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                                                             1602 TCCTCTCTTATGGATGAGTACTCAGA 1628
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                       LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTUANE: Datestin Poleso #1 00
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                                                                                                                       Conservative
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124..1326
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124..1326
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E: cDNA
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77.8%;
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Pred. No. 32;
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                                                                                                                                      Score 17.4;
Pred. No. 3
                                                                                                                       Mismatches
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APPLICANT: Boyle,
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                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                1602 TCCTCTCTTATGGATGAGTACTCAGA 1628
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                  TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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21;
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                                                                                                                     ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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CLASSIFICATION:
                                                                                                ZIP:
                                                                                                             COUNTRY:
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DEDNESS: single
DGY: linear
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Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
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Lacey, David L.
Calzone, Frank J.
                                                                                                             USA
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77.8%;
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Pred. No. 32;
O; Mismatches
                   Version #1.30
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APPLICATION NUMBER:

US/08/974,186

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US-08-795-446B-1
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                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boyle,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          MOLECULE TYPE: CDNA FEATURE:
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                SEQUENCE CHARACTERISTICS:
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LOCATION:
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CITY: Thousand Oaks
                                                          TOPOLOGY:
                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                              APPLICATION NUMBER:
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OCATION:
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nucleic acid
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1840 Dehavilland Drive
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Lacey, David L.
Calzone, Frank J.
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Chang, Ming-Shi
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77.8%;
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RESULT 14
US-08-706-945D-123
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08364081 Patent No. 5585464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SEQ ID NO 123
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TYPE: DNA
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (124)...(1326)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chang, Ming-Sn1
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                    ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No.
STREET: 9035 South 700
                                                              SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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STREET:
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                                                                                          MEDIUM TYPE: Diskette, 3.5 inch, COMPUTER: AST Advantage NB-SX20 OPERATING SYSTEM: DOS 6.2
                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                         COUNTRY: USA
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                  CLASSIFICATION:
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East, Suite
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Sequence 620, App
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ALIGNMENTS

PRIOR APPLICATION NUMBER: FR 99/03925 PRIOR FILING DATE: 1999-03-29 PRIOR PRILING DATE: 1999-03-29 PRIOR PRILING DATE: 1999-03-29 PRIOR PRILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin version 3.1 SEQ ID NO 15 LENGTH: 34 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: COTHER TANNOTHERS 밁 ş RESULT 1 US-09-963-803-15 US-09-963-803-15 Sequence 15, Application US/09963803 Publication No. US20030028922A1 GENERAL INFORMATION: APPLICANT: Meristem Therapuetics Query Match 100.0%; Score 34; DB 9; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 34; Conservative 0; Mismatches 0; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus FILE REFERENCE: 184332042 CURRENT APPLICATION NUMBER: US/09/963,803 CURRENT FILING DATE: 2001-09-26 OTHER INFORMATION: Guide desoxynucleotide building OTHER INFORMATION: block G1 1 GACTCCTCTACTTATCGATCGGTACTGTGAGACA 34 1 GACTCCTCTACTTATCGATCGGTACTGTGAGACA Length 34 Indels 0, Gaps 0

RESULT 2 US-09-738-626-619

Sequence 619, Application US/0
Publication No. US200201976053
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSH

Application US/09738626 o. US20020197605A1

MIZOGUCHI, HIROSHI

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; ORGANISM: Corynebacterium glutamicum US-09-738-626-620
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US-09-738-626-619
                                                                                                                                                                 SOFTWARE: Par
SEQ ID NO 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pa
SEQ ID NO 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 620, A Publication No.
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Best Local Similarity
                                 Matches
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                                                              Query Match
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CURRENT APPLICATION NUMBER: US/09/738;626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                  TYPE: DNA
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                                                Local
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1 GACTCCTCTACTTATCGATCGGTACTGTGAGA 32
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                               Similarity 75.(
24; Conservative
                                                                                                                                                                                  PatentIn ver. 3.0
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IKEDA, MASATO
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TATEISHI, NAOKO
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OCHIAI, KEIKO
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o. US20020197605A1
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75.0%;
                                              56.5%;
                             Score 19.2; D
Pred. No. 22;
0; Mismatches
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Pred. No. 21;
0; Mismatches
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Db 571214 GACTGCTCCTCTGATCGATCACTACGGTGACA 571245
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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US-09-738-626-1
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
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Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 62, Application US/10039785 Patent No. US20020067646A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PF550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Salcedo et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                 OR APPLICATION NUMBER: 60/341,237
OR FILLING DATE: 2001-12-20
OR APPLICATION NUMBER: 60/331,310
OR FILLING DATE: 2001-11-14
OR APPLICATION NUMBER: 60/331,044
OR APPLICATION NUMBER: 60/331,044
OR FILLING DATE: 2001-11-07
DR APPLICATION NUMBER: 60/327,364
DR FILING DATE: 2001-10-09
DR APPLICATION NUMBER: 60/323,807
DR FILING DATE: 2001-09-21
DR APPLICATION NUMBER: 60/309,176
DR FILING DATE: 2001-08-02
DR APPLICATION NUMBER: 60/294,981
DR APPLICATION NUMBER: 60/294,981
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FILING DATE: 2000-04-07
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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ZAKI, AKIO
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75.0%;
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Pred. No. 1.1e+02;
0; Mismatches 8;
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                                                                                                                                                                                                                                          JS-09-783-590-294
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Sequence 1, Application US/09939964
Publication No. US20030054522A1
                                                                                                                                                                       Matches
                                                                                                                                                                                                        Query Match
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SEQ ID NO 294
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOPTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (400)
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (327)
                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (141)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                   337 GAATTCTGAACTTTTCAAGGGGTACTGTGAG 367
                                                                                                                                                                                       Local Similarity
                                                                                                                                   1 GACTCCTCTACTTATCGATCGGTACTGTGAG 31
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74.2%;
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72.7%;
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                                                                                                                                                                                      Score 18.2;
Pred. No. 59;
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Pred. No. 4
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RESULT 9 US-09-946-807-1/c

Sequence 1, Application US/09946807 Patent No. US20020155144A1 GENERAL INFORMATION: APPLICANT: Stefansson, Hreinn

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CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compounds and methods to inhibit or TITLE OF INVENTION: augment an inflammatory response. FILE REFERENCE: 295.022US1
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauen Marie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/927,939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1997-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosenthal,
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ORGANISM: Rhizobium
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
1165 GARACCTCTACCCACCAATGGGAACTGGGAAACA 1132
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Perret, Xavier Philippe
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Pred. No.
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Pred. No. 2.4e+02
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RESULT 10
                                                                      Db 183456 GAATTCCCTATTTAATAATTGGTACTGGGAGAAA 183423
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                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                          Matches
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CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
                                                                                                                                                                                                                             LOCATION: (1)...(1531)
OTHER INFORMATION: n=a
                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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LOCATION: (1)...(1531)
OTHER INFORMATION: V=a
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LOCATION: (1)...(1531)
OTHER INFORMATION: k=g
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LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
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LOCATION: (1)...(1531)
OTHER_INFORMATION: s=g
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LOCATION: (1)...(1531)
OTHER_INFORMATION: m=a
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LOCATION: (1)...(1531)
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VAME/KEY: misc_feature
OCATION: (1)...(1531)
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OCATION: (1)...(1531)
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THER INFORMATION: y=t/u or
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                                                                                           1 GACTCCTCTACTTATCGATCGGTACTGTGAGACA 34
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OF INVENTION: HUMAN SCHIZOPHRENIA GENE
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Pred. No. 3.1e+02;
0; Mismatches 10
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US-09-795-686-1/c

Sequence 1, Application US/09795686
Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

FILE REFERENCE: 2345.2005-001

RESULT 11

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OTHER INFORMATION: n=a or g or c or t/u US-09-795-668-1
Db 183456 GAATTCCCTATTTAATAATTGGTACTGGGAGAAA 183423
                                                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
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TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
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                                                                                                                                                                                       OTHER INFORMATION: V=a
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                             1 GACTCCTCTACTTATCGATCGGTACTGTGAGACA 34
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                                                          Score 18; DB 10;
Pred. No. 3.1e+02;
0; Mismatches 10
                                                              10;
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RESULT 12
US-09-918-995-30042
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                                                                 APPLICANT: Hyseq, Inc.
APPLICANT: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
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Publication No. US20030073623A1
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                                NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windo
SEQ ID NO 30042
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CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
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OTHER INFORMATION: h=a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: b=g
NAME/KEY: misc feature
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OTHER INFORMATION: m=a or c
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LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or
NAME/KEY: misc feature
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TYPE: DNA
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LOCATION: (1)...(1531)
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                                                      PastSEQ for Windows Version 3.0
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Pred. No. 3.1e+02;
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, App
Publication No.
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APPLICANT:
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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-12-19
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FILING DATE: 1997-09-19
APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-19
APPLICATION NUMBER: 60/059836
                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-09-17
APPLICATION UMMBER: 60/059122
FILING DATE: 1997-09-17
APPLICATION UMMBER: 60/059184
FILING DATE: 1997-09-17
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FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
                          APPLICATION NUMBER: 60/062814
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24
                                                                                        FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17
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FILING DATE: 1997-09-18
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APPLICATION NUMBER: 60/062250
APPLICATION NUMBER: 60/063045
FILING DATE: 1997-10-24
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Watanabe, Colin K
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70. US20030004311A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood,William
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Pred. No. 89;
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RILING DATE: 1997-10-31
APPLICATION NUMBER: 60/0
FILING DATE: 100-1

APPLICATION NUMBER: 60/ FILING DATE: 1997-10-29

APPLICATION NUMBER: 60/063561 APPLICATION NUMBER: 60/063550

1997-10-28 1997-10-

60/063704

FILING DATE: APPLICATION NUMBER:

1997-10-27

60/063329

1997-10-

60/063327 60/063127

APPLICATION NUMBER: 60/063735

FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063733

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OR FILING DATE: 19/98-06-11
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR FILING DATE: 1998-06-29
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR APPLICATION NUMBER: 60/09045
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090538
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090538
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OR APPLICATION NUMBER: 60/084637
OR APPLICATION NUMBER: 60/084637
OR PILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/085149
OR APPLICATION NUMBER: 60/08533
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085339
OR APPLICATION NUMBER: 60/085697
OR APPLICATION NUMBER: 60/085697
OR APPLICATION NUMBER: 60/085697
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/086414
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086414
OR APPLICATION NUMBER: 60/086414
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086410
OR FILING DATE: 1998-05-20
OR APPLICATION NUMBER: 60/086410
OR APPLICATION NUMBER: 60/086026
OR FILING DATE: 1998-05-06-10
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088910
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DR APPLICATION NUMBER: 60/082999

DR FILING DATE: 1998-04-24

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/083545

DR APPLICATION NUMBER: 60/083645

DR FILING DATE: 1998-04-29

DR APPLICATION NUMBER: 60/084600

DR FILING DATE: 1998-05-07

DR FILING DATE: 1998-05-07
                                                                                                                                                                                                                                             FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
                                                                                APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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Length 3371;
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Query Match 52.4%; Best Local Similarity 75.9%; Matches 22; Conservative Score 17.8; DB 9; Pred. No. 1.4e+02; 0; Mismatches 7 Indels 0 Gaps

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OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081695
OR FILING DATE: 1998-04-14
OR APPLICATION NUMBER: 60/081817
OR APPLICATION NUMBER: 60/081817
OR FILING DATE: 1998-04-15

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1998-02-27

60/079728

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1998-03-31 1998-03-27

60/080165

APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20

APPLICATION NUMBER:

1998-03-25 1998-03-20

60/079663

60/079294

APPLICATION NUMBER: 60/074092 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12

APPLICATION NUMBER: 60/073612 FILING DATE: 1998-02-04

APPLICATION NUMBER:

1998-02-09

60/074086

APPLICATION NUMBER:

FILING DATE:

1998-01-23

60/072320

APPLICATION NUMBER: 60/069694

1997-12-16

FILING DATE: 1997-12-1: APPLICATION NUMBER: 60/069334

APPLICATION NUMBER: 60/069278 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069212 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER:

FILING DATE: 1997-11-2

APPLICATION NUMBER: 60/066364 APPLICATION NUMBER: 60/065846 FILING DATE: 1997-11-17 FILING DATE: 1997-11-

FILING DATE:

APPLICATION NUMBER: 60/066511

1997-11-24

60/066453

FILING DATE: 1997-11-24

APPLICATION NUMBER: 60/064809 FILING DATE: 1997-11-07 APPLICATION NUMBER: 60/064248 FILING DATE: 1997-11-03 APPLICATION NUMBER: 60/063755

APPLICATION NUMBER: 60/065186

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US-10-123-904-35/c
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; ORGANISM: Homo Sapien
US-10-121-049-35
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 35
LENGTH: 3371
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                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin P.
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Publication No. US20030022328A1
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Best Local Similarity 75.5
Matches 22; Conservative
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                                                                                    APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT APPLICATION NUMBER: US/10/121,049
Prior Application removed - See File Wrapper or Palm
Prior Application removed - See File Wrapper or Palm
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ICANT: Zhang, Zo
E OF INVENTION: S
E OF INVENTION:
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                                                                                                    Stewart, Timothy A.
                                                                                                                      Smith, Victoria
                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Gerritsen, Mary E.
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Godowski, Paul J.
Gurney, Austin L.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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                                                  Wood, William
                                                                  Watanabe, Colin K
SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
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75.9%;
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Pred. No. 1.4e+02;
0; Mismatches 7;
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                                                                  Matches
                                                                                   Query Match 52.4%;
Best Local Similarity 75.9%;
                                                                                                                                                                                                        SEQ ID NO 35
                                                                                                                                                                                                                      FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                    LENGTH: 3371
TYPE: DNA
ORGANISM: Homo Sapien
3291 CTCTATCTACCCATCTGTACTTAGAGACA 3263
                              6 CTCTACTTATCGATCGGTACTGTGAGACA 34
                                                                  22;
                                                                    Conservative
                                                                                                                                                                                                                                            See File Wrapper or Palm
                                                                  0;
                                                                                   Score 17.8; DB 9;
Pred. No. 1.4e+02;
                                                                  Mismatches
                                                                                                      DB 9;
                                                                                                   Length 3371;
                                                                    Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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34
1 gactcctctacttatcgatcggtactgtgagaca 34
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2:*
gb_htc:*
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em_gss_pln:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20	20.2	20.4	20.4	20.8	21.2	Score
58.8	59.4	60.0	60.0	61.2	62.4	Query
136	702	660	599	589	665	Query Match Length DB
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BG833308	BI823138	BQ109731	BI672108	BM096067	AZ607800	ult Query No. Score Match Length DB ID
	BI823138 603039579		BI672108 ft34f03.x	BM096067 fv30c09.x		Description

ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AZ607800 LOCUS DEFINITION
University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00	plasmid inserts Unpublished (2000) Contact: Robert B. Weiss	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 665) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,	CIONE UUGCIMU43UMZZ F, DNA SEQUENCE. AZ607800 AZ607800.1 GI:11729990 GSS. house mouse. Mus musculus	AZ607800 665 bp DNA linear GSS 13-DEC-2000 1M0430M22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

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VERSION
KEYWORDS
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AUTHORS
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similar to
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Wylie, T., Un, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Un, S., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Schurk, R., Ritte: Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritte: Schu, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watersind, M., S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watersind, M., S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watersind, M., Watersind, M., McCann, R., Watersind, M., Water
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                     Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                              WashU Zebrafish EST Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                 and Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei;
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quality sequence stop: 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competents. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. Coli_strain_XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0430M22"
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Ostariophysi; Cypriniformes
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BI672108/c
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                                                           Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                          Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@atmage.llnl.gov zebrafish identity (p-value greater than 1e-99) found to: gi[2446832|gb|AA606179|AA606179 fal6e02.sl Appel Eisen zebrafish
                                                                                                                                                                                                  and Wilson, R.
WashU Zebrafish EST Project 1998
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The library was constructed by Dr. 2. Gowashington University Genome Sequencing
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                                             Email: zbrafish@watson.wustl.edu
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Location/Qualifiers
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/dev stage="adult"
/lab_host="DHIOB (phage resistant)"
/lab_host="DHIOB (phage resistant)"
/note="vector: pME18S-FL3; Site_1: DTAILI (CACCATGTG);
Site_2: DTAILI (CACTGTGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DTAILI adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DTAILI
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed and donated by Dr. Sumio
Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CGACCTGCAGCTCGAGCTACA."
25 a 145 c 172 g 147 t
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/sex="male"
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78.1%;
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Pred. No. 3.
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Gong. DNA Sequencing by:
ng Center St. Louis. Please
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                                                               Email: help@image.llnl.gov
This read has been produced as part of the I.M.A.G.E. Consortium quality read has been produced as part of the I.M.A.G.E. Consortium quality read has been produced as part of the I.M.A.G.E. Consortium quality read to the sequence as having 100 or more base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For info@image.llnl.gov.

Plate: LLAM11377 row: k column: 6
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Prange, C.K.
The I.M.A.G.E. Consortium quality control effort
                                                                                                                                                                                                                                                                                                                          Lawrence Livermore National Laboratory
                                                                                                                                                                                                                                                                                                                                                       The I.M.A.G.B. Consortium
                                                                                                                                                                                                                                                                                                                                                                             Contact: Prange CK
                                                                                                                                                                                                                                                                                                                                                                                                    resequencing for verification 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Cyprinidae; Danio.
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Actinopterygii; Neopterygii; Teleostei;
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                                            primer: -21m13
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                     quality sequence stop: 660
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(http://genome.wustl.edu/est/lambda_protocol.shtml).
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on Please contact Zhiyuan Gong for further information on this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Roa Singapore 11936)."

Singapore 11936)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Gong zebrafish testis"
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lab_host="DH10B (phage-resistant)"
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Pred. No. 4.6e+02;
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Ostariophysi; Cypriniformes
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603039579F1 NIH_MGC_115 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 702)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11450 row: m column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."

8 C 127 g 228 t
/note-"Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); Rt source anonymous pool of 6 male brains, age 69 range 23-27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and
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/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: testis (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the testes of 31 male adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                               /clone="IMAGE:5180730"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/db_xref="taxon:7955"
/clone="IMAGE:5152637"
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80.0%;
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Pred. No. 4.8e+02;
0; Mismatches 6
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                                CCTCTACTTATCGATCGGTACTGTGAGA 32
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BG833308.1
EST.
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Email: walbot@stanford.edu
Plate: 951004 row: F column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG833308
951004F05.x2 951 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clade; Panicoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mayв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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650 725 8221
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                                                                                                                                  (Promega). cDNA was synthesized using both formers in separate reactions and equipped with coligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

35 c 31 g 36 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enriched for full-length clones and was construc
Gruber (Invitrogen).. Research Genetics tracking
021. Note: this is a NIH MGC Library."
155 c 160 g 178 t
                                                                                                                                                                                                                                                                                      /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; T
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis S
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/cultivar="BMS (Black Mexican Sweet)"
/cultivar="BMS (Black Mexican Sweet)"
/db xref="ftaxon:4577"
/clone_lib="951 - BMS tissue from Walbot Lab (GR)"
/tissue_type="suspension culture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              dev_stage="mixed logarithmic and stationary growth
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                                                                                  58.8%;
82.1%;
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BMS tissue
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                                                                Score 20; DB 12;
Pred. No. 4.3e+02;
D; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.2; DB 1:
Pred. No. 5.9e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA libraries sequenced at Stanford
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Walbot
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                                                                                                Length 136;
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Lab (GR)
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Zea mays cDNA,
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59 N

ACTCCTCTACTTATCGATCGGTACTGTGAGA 32 ACTOTTOTATTTAACGAGTGGTAATGTGACA 29

Matches Query Match Best Local (

Similarity

58.2%;

Score 19.8; D Pred. No. 6.9e 0; Mismatches

9e+02 멂

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KEYWORDS
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BF542321/c
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MEDLINE
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UI-R-C2p-se-d-06-0-UI.rl UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-se-d-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone dist
clones will be available through Research Genetics
This clone is also available through the I.M.A.G.E.
LLNL (info@image.llnl.gov). IMAGE ID= 1768584
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9),
97044477
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Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
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                           121
                                                                                                                                                                     /note="Wector: pr773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Boo RI; The UI-R-C2p library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified CDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography.
                           791-806,
1 88 c
                                           converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6 791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares,
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="UI-R-C2p-se-d-06-0-UI"
/clone_lib="UI-R-C2p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Consortium at
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Best Local (
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                                                                                                        137 TGCTCTTATCGATAGGTCTTGTGAAATA 107
                                                                                                                                         4 TCCTCTACTTATCGATCGGTACTGTGAGACA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Ettenne-Pascal Journet, Laboratoire
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castamet-Tolosan Cedex, Françe (Email:
Mt-est@toulouse.inra.fr Website:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             barrel medic.

Medicago truncatula

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; edaceae; Papillonoideae; Trifolieae;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)
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AL387696.1 GI:9687447
EST.
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                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 451)
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                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil: 2/3 calcined ferragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8). The plants were watered every day and twice a week with a modified nutrient long mahton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. CDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Strategene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exassit helper phage and propagated in SOIR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of
                                                                                                                                                                                                                                                                                                                                          b
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dev_stage="harvested 3 weeks post inoculation with Glomus/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="MtBC"
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77.4%;
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                                                                                                                                                                                                                                       Score 19.8;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                          106 g
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Chatagnier,O., Kahn,D., Gianinazzi-Pearson
                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                       7.4e+02
                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                          Length 451;
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Query Match Best Local (Matches

Similarity

58.2%; 77.4%;

Score 19.8; Pred. No. 7 Mismatches

.7e+02 DB 13;

Length

502;

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Conservative

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SOURCE
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                             BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0649 row: B column: 07
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Luo,A.,
Tanaka,T., Kunath,T., Rossant,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Trophoblast Stem Cell cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 502)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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                             103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 1154199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lumenfeld Research Institute, Canada). Double-stranded
                                                                                                                                     4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B B. coll host was transformed with the ligation mixture by the crandary decrease.
                   mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao (NIA)."

136 c 148 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Trophoblast stem cell"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="B5/EGFP transgenic ICR mice"
/db_xref="niaEST:CO649B07-3"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                    BB764031 RIKEN full-length enriched, B16 CDNA clone G370032F11 3', mRNA sequence.
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H4059D12-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4059D12 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuya, Y., Kon, M., Kawai, J., Kojima, K., Numasaki, R., Okazaki, Y., Ok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yong Qian
Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Drive, Suite 3000, Baltimore, MD 21224-6820, USA
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                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 524)
                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                 BB764031.1
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1 (bases 1 to 514)
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clone is among a rearrayed set of
than 20 cDNA libraries."
a 142 c 148 g 118 t
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/db_xref="taxon:10090"
/clone="H4059D12"
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/lab_host="DH10B"
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/strain="C57BL/6"
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Rodentia;
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Rodentia;
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Pred. No. 7.7e+02;
0; Mismatches
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i, B16 F10Y cells
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Imotani,K., Ishii
,M., Matsuyama,T.,
azaki,Y., Okido,T.
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Mus musculus

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                                                                               BB752196
BB752196 RIKEN fu:
clone G270012B20 :
BB752196
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Pujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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                                                      BB752196.1
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house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db xref="taxon:10090"
/clone="G370032F11"
/clone lib="RIKEN full-length enriched, B16 F10Y cells"
/clone lib="RIKEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
/note="pooled tissues; (tissue_type=cerebellum,
/note="pooled tissues; (tissue_type=cerebellum,
/cell_type="B16 F10Y cells"
/note="pooled tissues; (tissue_type=mixed),
/tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=mixed), (tissue_type=hippocampus, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                      GI:16200663
                                                                                                                                                                                                                                                                                                                                                                                                                          58.2%;
                                                                                                     full-length enriched,
20 3', mRNA sequence.
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                                                                                                                                               ACCTCTCTATTTATCTGTCTGTGCTGAGA 79
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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  AZ331947
                                                                                                                                                                                                                                                       Similarity 77.4
24; Conservative
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Fax: 81-45-503-9216
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Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                 dev stage=16 days neonate, sex=mixed); (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=mixed); (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed); (tissue_type=lung, dev_stage=13 days embryo, sex=mixed); (tissue_type=lung, dev_stage=13 days embryo, sex=mixed);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="melanocyte"
note="pooled tissues; (tissue_type=cerebellum,
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/clone_lib="RIKEN full-length enriched, melanocyte"
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                                                                                                                                                                                                                                                                                  58.2%;
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  596
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  DNA
                                                                                                                                                                                                                                                                                                             Length 530;
linear
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GSS 29-SEP-2000
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188
                                           2 ACTCCTCTACTTATCGATCGGTACTGTGAGA 32
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Insert Length: 10000 Std Erry
Plate: 0060 row: J column: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       Similarity
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                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                         adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

174 c 163 g 118 t
                                                                                                                                                                                                                                                                                                             10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The constant was signed to the blunt ends in high molar excess.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                  58.2%;
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                                                                                                                     Score 19.8; DB 1'
Pred. No. 8.1e+02
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                                                                                              Mismatches
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RESULT 14 AZ831669 LOCUS

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                                                                                                                                                                                                Query Match
Best Local Similarity 77.4
24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0111 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 611)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nouse mouse
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 611.
                                                                                                                                                                                                                                                                                                                                     was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC2M0111H02"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                    Score 19.8; DB 17;
Pred. No. 8.2e+02;
0; Mismatches 7;
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Search completed: May 11, 2003, 04:54:25 Job time: 550.556 secs

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527
                                                                                                                                                                                                                               Local
                                                                                  2 ACTCCTCTACTTATCGATCGGTACTGTGAGA 32
ACCICICIATITATCIGICIGIGAGA 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UI-M-EM0-bvj-f-05-0-UI.rl NIH BMAP_EM0 Mus musculus cDNA clone IMAGE:5692804 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: NGC clone distribution information can
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Oligo-dT primer containing a Not I site. Double stranded CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, dispested with Not I, and then clomed directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="NIH BMAP EMO"
/clone lib="NIH BMAP EMO"
/tissue_type="whole brain"
/dev stage="embryo 18.5 dpc"
/lab_host="DH1OB (T1 phage resistant)"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to the content of the conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an
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/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                      Length 615;
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JOURNAL AX036750 Sequence AX036750 synthetic construct artificial sequences. artificial sequences. 1 (bases 1 to 33) Rance,I., Theisen,M. and Gruber,V. Chimeric expression promoters originating is mottle virus and cassava vein mosaic virus patent: WO 0058485-A 16 05-OCT-2000; synthetic construct. AX036750.1 16 from Patent GI:11226259 33 bp WO0058485. DNA from commelina yellow linear PAT 16-NOV-2000

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Direct Submission
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 132770 bases at least Q40
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Consensus quality: 144434 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Muridae; Murinae;
2 (bases 1 to 31069)
Worley, K.C.
Direct Submission
Submitted (09-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: hgsc-helpsbcm.tmc.edu

------- Project Information

Center project name: KANI

Center clone name: CH230-50A6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae DNA from 2R chromosome, clone 11N17.
Au439060
Au4390601 GI:19577369
11N17.1.1 gene; 11N17.10 gene; 11N17.11 gene; 11N17.12 gene;
11N17.13 gene; 11N17.14 gene; 11N17.15 gene; 11N17.16 gene;
gene; 11N17.3 gene; 11N17.4 gene; 11N17.5 gene; 11N17.6 gene;
11N17.7 gene; 11N17.8 gene; 11N17.9 gene; 4F11.10 gene; 4F11.9
gene; acetyltransferase; cell-adhesion protein; chitin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomasova, D., Ton, L.Q., Copley, R.R., Zdobnov, E.M., War Hong, Y.S., Sim, C., Bork, P., Kafatos, F.C. and Collins, F Comparative genomic analysis in the region of a major Plasmodium-refractoriness locus of Anophelesgambiae Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8179-8184 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-MAR-2002) Thomasova D., I
Activities, European Molecular Biology
1, Heidelberg, 69117, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; cytoskeletal regulator; deoxynucleoside kinase; FGF-signaling promoter; protein; ribosomal protein; sRNP; tachykinin receptor; transcription factor; translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomasova, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                African malaria mosquito.
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/Translation="MLVISQOPTASSSTTSSSSKPSPOOQOQLHSADVPHSSTSOSS
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VCRGANGATAASDACLECTLAVEBHERQPYELTVEASSDRGLSVHGPTELGVLVRPMHP
RVTCAMDHAGELASDLYALYDEQLDRCMRTGTTHHBADA I BCTFYCEPDF IVLLELC
KLRKETELRALERLSTQRTKRDFHPTGGSLNNLLSTHHBADA I BCTFYCEPDF IVLLELC
KLRKETELRALERLSTQRTKRDFHPTGGSLNNLLSTHHBADA I BCTFYCEPDF IVLLELC
STIFLVTDULGEFYNRALAANANGLTYDRAGKSVPGGSDSAPPKSNPPLEVILLOTIKH
QILHKLGLRERPRLTKHLNNEHVFEAFDR I YGNKINIGNTYABEHYYRRYLTANLSSD
                                                                                                                                                                                                                                                                                                    join(640. .654,1576. .1893,2259. .3527,4487.
4890. .5087,5160. .5267,5343. .5465)
                                                                                                                                                                                                                                                                                                                                                join(640 .654,1576 .1893,2259 .3527,4487.
4890 .5087,5160 .5267,5343 .5465)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 540. .5465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Anopheles gambiae"
|strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:7165"
chromosome="2R"
                                                                                                                                                                                                                                                                                                                                                                                                                    gene="4F11.9"
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DNA from 2R chromosome,
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ssisrsrstvvnsynlttcpswahapngpcrht"
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ELLETWERLFAVRLRLEESYDFAKKALVNLMNKYGDSKSQRNIFNYPYNLKLMIKOVI
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/gene="4F11.9"
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/gene="4F11.9"
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                                                                  l Similarity 81.8%;
27; Conservative
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TNPFRTSTSKEDEALGALGPLHRLLSSNVRSLGNSVHSGRSTPRELLESSQPAGG
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LKKSKESAATRPKDQPGGGSPASSSGMAILDMSASPKMYSFRRIAQQGGYGGSPTKGA
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KOQDIDDFNIHDTTLARQPSVGGSRRRGGSTTDREKRLSHDRKPSYSSSERSSTGILG
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DRYDHLLPSPAEQCRILASKPAETIKIDTSGRAFDENSSTRKSLVCYTTTROKKEGD
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PVRASGKAPESESGGGGGVVEETISSFKENIFLKEDENNFMRGEVPRMTKSFAGFSTV
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Direct Submission

Submitted (12-MAR-2001) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Bevan, M., Murphy, G., Ridley, P., Hud
Rudd, S., Lemcke, K. and Mayer, K.F.X.
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LDITDLDKLTDKSLEFITEGCRYLKSLKLTSNRFSDECIAAFLEVSGGSLRELCLNKV
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Contains Myb DNA-binding domain repeat signatures
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FSFSLLLLLLILAIALSLYSDPSLTRFDPYWIHRLCGSFGGLLVILILLVFVLICKAS
                                                                                                                                                                                                                                                                          complement (9801. .10177)
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LILLPPVADSVKLIQDFHQSLISATEKFKGFILNSLASKNPLFQEAVRLSSEFHILCDE
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APPAIVNPLSTLCDPYLNIFRGFIPPLGGLDLSPILAFLVLNAFTSSAMALPCELPSA
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Arabidopsis thaliana"
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complement(join(9068.
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AC021316 173535 bp DNA linear PRI 23-AUG-2
Homo sapiens chromosome 15, clone RPI1-11J16, complete sequence.
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                                                                                                                                                                                                                           Conservative
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GETEPVDGSVLAGRSVVDESMLTGESLPVFKEBGCSVSAGTINMDGPLRIKASSTGSN
STISKIVRMVEDAQGNAAPVQRLADAIAGPFVTIMSLSAMTFAFMYYVGSHIFFPUL
LNDIAGPDGDALALSLKLAVDVLVSCPCALGLATFTALLIGTSLGAKRGYLIRGGDV
LERLASIDCVALDKTGTLTEGRPVVSGVASLGYEEQEVLKMAAAVEKTATHFIAKAIV
MEAESLAYLKTPETRGQLTEPGFCTLAEIDGRFVAVGSLEMVSDRFLKKXDSSDMVKLE
SLLDHKLSNTSSTSRYSKTVVYVGREGGGIGAIAISDCLRQDAEFTVARLQEKGKT
VLLSGDREGAVATVAKNVGIKSSSTNYSLSPEKKFEFISNLQSSGHRVAMVGDCINDA
PSLAQADVGIALKIEAQENAASNAASVILVRNKLSHVDALSLAQATMSKVYQNLAWA
PSLAQADVGIALKIEAQENAASNAASNILVRNKLSHVDALSLAQATMSKVYQNLAWA
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LCCGSHTSHILHSLGIHIAHGGIWDLLHNSYVKGGLAVGALLGPGRELLFDGIKAFGK
RSPNMNSLVGLGSMAAPSISLISLVNPELEWDASFFDEPVMLLGFVLLGRSLEERAKL
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                                                                                                                                                                                                                                                                                                                                        12462.
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/gene="At5g21930"
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ITSDTPILLDVSGmMCGGCVARVKSVLMSDDRVASAVVNMLTETAAVKFKPEVEVTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAC34486.
/db_xref="GI:13374852"
                                                                                                                                                                                                                                                                                                              /gene="At5g21930"
                                                                                                                                                                                                                                                                                                                                                                                                         12375.
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|gene="At5g21930"
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                                                                                                                                                                                                                                                                                                                                                                               gene="At5g21930"
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CE 4 (bases 1 to 173535)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalla, K., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Menthews, C., Liu, G., MacLean, C., Macdonald, P., Major, J., Metthews, C., Liu, G., MacLean, C., Macdonald, P., Major, J., Minova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L4301
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                 /rpt_family="LTR55"
complement(19119. .19164)
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17239
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complement(7827. .1
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/rpt family="L1"
complement (2304. .3709)
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|5215. .15519
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clone_lib="RPCI-11 Human
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ob_xref="taxon:9606"

chromosome="15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lement (4523. .4779)
family="Tigger3 (Golem)"
Lement (4777. .4866)
                                                                                                                                                          _fami
                                                                                                                                                                                                                                                                                                                                                     family="LIPA7"
                                                                                                                                                                                                                              _fami
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lement (4182. .447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="L1PBa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="AT_rich"
                                                                                      family="L2"
                                                                                                                        family="L1MA4"
                                                                                                                                                                                          family="MLT1E2"
                                                                                                                                                                                                                                                                fami
                                                                                                                                                                                                                                                                                                                                   family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                      family="Tigger3(Golem)"
ement(5350. .5474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="(TA)n"
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   .19462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ily="AluSc"
                                                                                                                                                                                                                                                               .ly="AluJb"
                                                                                                                                                        .y="L1ME3"
                                                                                                                                                                                                                             y="L1ME3"
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KEYWORDS
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AC107787
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                ORGANISM
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                              pieces.
AC107787.2 GI:20143689
AC107787.2 GI:20143689
HTG; HTGS_PHASE2; HTGS_DI
Mus musculus.
                                                                                                                                                                                                                                                                                               27;
                                                                                                                      AC107787 194974 bp Mus musculus clone RP23-432F10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                               70.9%;
Similarity 81.8%;
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                /note="<30 qual SNGL region"
complement (24818. 24838)
/note="<30 qual SNGL region"
complement (24862. 24870)
/note="<30 qual SNGL region"
complement (25087. 25675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (24731...24735)
/notes "430 qual SNGL region"
/notes "430 qual SNGL 76910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (23589. .2359)

/note="<30 qual SNGL region"

complement (23619. .23623)

/note="<30 qual SNGL region"

23639. .23815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (24459 . .24782) / rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="<30 qual SNGL region"
complement(22279. .22409)</pre>
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/note="<30 qual SNGL region"
complement (22262. .22271)
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19463. .19537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(24783. .:/rpt_family="AluSg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AluJb"
23234. .23302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (24802
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complement(20765. .210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TA)n"
complement(19538. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="L1ME3"
[ement(24458)
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7. .22064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="MLT1J1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="(CATATA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family="MLT1J2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="(CATATA)ก"
                                            HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                               Score 23.4; DB Pred. No. 1.1e+C
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .24812)
                                                                                                                      DNA linear HTG 12-APR-2002 WORKING DRAFT SEQUENCE, 34 ordered
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamaat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riisy, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talanas, J., Tesfaye, S., Theodore, J., Thopham, K., Talanas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembsk, L., Zimmer, A. and Zody, M.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Collaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Chararo,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
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Birren,B., Linton,L., Nusbaum,C., Lander,B., All,A., All,A., All,A., All,A., All,A., Barren,B., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Anderson,S., Barna,N., Campopiano,A., Chang,J., Chazaro,B., Brown,A., Camarata,J., Campopiano,A., Collymore,A., Cook,A., Collymore,A., Cook,A., Collymore,A., Cook,A., Collymore,A., Collymore,A., Cook,A., Collymore,A., Coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 12, 2002 this sequence version replaced gi:18308489. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fat Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyn, S., Fatzhar, R., Charata, B., Carana, S., Fatzhar, R., Carana, B., Carana, S., Fatzhar, R., Carana, R., Carana, S., Fatzhar, R., Carana, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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(bases 1 to 194974)
                                          Center clone name: 432 P 10
------ Summary Statistics
Sequencing vector: Plasmid, n/a, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L20471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Assembly program:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linton, L., Nusbaum, C. and Lander, E. us, clone RP23-432F10
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provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consists of 34 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 185565 bases at Consensus quality: 188852 bases at Consensus quality: 190073 bases at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 8.9 in Q20 bases; agarose-fp Quality coverage: 9.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 210000; agarose-fp
Insert size: 191674; sum-of-contigs
                                                                                                                                                       66978
                                                                                                                                                                                                      57186
60204
60304
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                                                                                                                                                                                            63083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 2455: gap of 100 bp
3109: contig of 654 b
10 3209: gap of 100 bp
0 4151: contig of 942 b
2 4251: gap of 100 bp
4930: contig of 679 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 7896: gap of 100
7 9525: continuodical 100
7 9525: continuodical 100
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7796: c
                                                                                                                                                                                                                                                                      5471
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              102369:
                                       94885;
                                                                88946:
                                                                                        82180:
                                                                                                                 77947:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    9625: gap of 100 bp
10896: contig of 1271 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a 'working draft' sequence.
                                                                        7947: gap of 10
82080: contig of 0
2180: gap of 10
88846: contig of 0
                                                                                                                                                                                                    0303: gap of
63082: cont
                                                                                                                                                                                                                                                                                                                                                         126: gap of 10
45197: contig of 3
3297: gap of 10
47519: contig of 2
                     885: gap of 100 bp
102269: conjig of 7384
                                                                                                                                                                                                                                                      050: gap of 100 bj
54612: contig of 2562
712: gap of 100 bj
57085: contig of 2373
                                                                                                                                                                            .82: gap of 1
66877: contig of
                                                                                                                                                                                                                                                                                                           798: gap of 51950: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp arigith 123: contig of 1093 bp in length 100 bp 6989: contig of 6989: contig of
                                                  94785: contig of 5839
                                                                                                                         77847: contig of
                                                                                                                                                 71786: contig of 4809
                                                                                                                                                                                                                                                                                                                                    19: gap of 49698: con
                                                                                                                                                                                                                                                                                                                                                                                                          13026: contig of 2030 l
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1021: contig of 1021 bp in length
9: gap of
)158: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989: contig of gap of
                                                              gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 100 bp
contig of 1629 bp
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                                                                                                                                                                                                                               contig of 3018
 100 bp
of 7789 bp
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REFERENCE
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AC091229/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTTGTTATTTTTCATCTTCCATTGCAGCAA 49951
natuus.
1 (bases 1 to 336062)
1 (bases 1 to 336062)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ali-osman, F.R., Ali-osma
                                                                                                                                                                                                                                                                                                                                                                                                                                 336062 bp
Rattus norvegicus clone CH230-1A3,
185 unordered pieces.
                                                                                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1.
                                                                                                                                                                                  Rattus.
                                                                                                                                                                                                                                                                                                                                                                                 AC091229.11 GI:21953795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193613 193712: gap of 193713 194974: conti
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clone_end:SP6
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13127. .45197
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/db_xref="taxon:10090"
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1707. .2355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.9%; Score 23.4; DB 2;
81.8%; Pred. No. 1e+02;
tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10896
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N PROGRESS ***,
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COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently consists of 185 contigs. The true order of the pieces

It currently the ...

consists of

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Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, D., Hober, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, B., Kelly, S., Khan, U., King, L., Kovavah, J., Kovava, C.,
Karlsson, B., Kelly, S., Khan, U., King, L., Kovavah, J., Kovava, C.,
Karlsson, B., Kelly, S., Khan, U., King, L., Kovavah, J., Kovava, C.,
Karlsson, B., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R. J., Lu, X., Lucler, A., Lucler, R., Juna, R., Wa, J.,
Lozado, R. J., Lu, X., Lucler, A., Lucler, R., Luna, R., Wa, J.,
Maseey, E., Mashiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwnonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, B., Pu, L.L., Qulles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Walliamson, A., Waeren, R., Washington, C., Watlington, S.,
Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D.,
Unnublished
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Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Davlor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-APR-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 336062)
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On Jul 24, 2002 this sequence version replaced gi:20976487
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Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 37% of reads
Chemistry: Dye-terminator Big Dye: 63% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 151384 bases at least Q40
Consensus quality: 169228 bases at least Q20
Consensus quality: 178295 bases at least Q20
                                                                                                                                                                                                                                                                                                  Center project name: TUAJ
Center clone name: CH230-1A3
Center clone name: CH230-1A3
Center Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R.:, Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R.:, Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, B., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorme, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
                                                                                                                                                                              345243 bp
Rattus norvegicus clone CH230-1B12,
108 unordered pieces.
AC091347
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27; Conserv
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 24, 2002 this sequence version replaced gi:20162995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley,K.C.
Direct Submission
Submitted (18-APR-2001) Human Genome Sequencing Center, Department Submitted (18-APR-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 345243)
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                                                                                                                                                                                                                                                                                            Center project name: TUDB
Center clone name: CH230-LB12
Center clone name: CH230-LB12
Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Sequencing vector: M13;
Sequencing vector: Bodipy: 33% of reads
Chemistry: Dye-terminator Big Dye: 67% of reads
Chemistry: Dye-terminator Big Dye: 67% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 258903 bases at least Q40
Consensus quality: 258903 bases at least Q20
                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a "working draft" sequence. It currently consists of 108 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web
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Center: Washington University Genome Sequencing Center code: WUGSC center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
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                                                                                                                                 Parkway,
                                                                                                                                                Submitted (13-AUG-2002) Genome Sequencing Center, 4444 Forest
                                                                                                                                                                                   Submitted (27-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 177899) MCPherson,J.D. and Waterston,R.H.
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McPherson, J.D. and Waterston, R.H.
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McPherson, J.D. and Waterston, R.H.
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Mammalia; Eutheria; Rodentia;
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Mus musculus chromosome 10 clone RP24-545017, complete sequence.
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Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:15795440.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
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Human DNA
                     http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-431K17 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-445P19 is at 58922 in this
sequence. The true right end of clone RP11-108M21 is at 2000 i
this sequence.
                                                                                                                                                                                                                                                                                                                                                  assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 mapping Group. Further information can be found at
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BASE COUNT
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AC124546
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                                                                                                               Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 223625 bases at least Q40
Consensus quality: 224098 bases at least Q30
Consensus quality: 224340 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 224760; sum-of-contigs
Quality coverage: 11.52 in Q20 bases; agarose-fp
Quality coverage: 11.90 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTGTTACTTTTCTTCTATTCCAGCCA 33
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Mammalia; Eucheria; Rodentia; Sciux
1 (bases 1 to 224860)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
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                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkway, St. Louis, MO 63108, USA
On Aug 11, 2002 this sequence version replaced gi:21426675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-AUG-2002) Genome Sequencing Center, 4444 Forest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-JUN-2002) Genome Sequencing
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McPherson, J.D. and Waterston, R.H.
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AC124546.2 GI:22203919
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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nilarity 83.9%;
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/clone_lib="RPCI-11.2"
11328 c 10604 g 19
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/db_xref="taxon:9606"
/chromosome="1"
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Pred. No. 1.7e+02;
0; Mismatches 5;
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AC124707/c
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Sequencing vector: M13; 0$
Sequencing vector: M13; 0$
Sequencing vector: plasmid; 100$
Chemistry: Dye-primer ET; 0$ of reads
Chemistry: Dye-terminator Big Dye; 100$ of reads
Chemistry: Dye-terminator Big Dye; 100$ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 285901 bases at least Q40
Consensus quality: 285901 bases at least Q30
Consensus quality: 28883 bases at least Q20
Insert size: 197000; agarose-fp
                                                                                                                                                                                                                  Center project name: M_BB0073H16
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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McPherson, J.D. and Wat
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The sequence of Mus musculus clone
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ilarity 83.9%;
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db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Waterston, R.H.
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291588 bp DNA linear HTG 22-JUN-2002
Mus musculus chromosome UNK clone RP24-73H16, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
                       Genter: Washington University Genome Sequencing (Center: Washington University Genome Sequencing (Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                            Submitted (15-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (Dases 1 to 291588)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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cure 7606. .224860
/note="assembly_name:Contig6"
72803 a 40558 c 41158 g 70219 t
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7605: gap of unknown length
224860: contig of 217255 bp in length
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; Pred. No. 1.4e
0; Mismatches
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). 1.4e+02;

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VERSION
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AL731717
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                                                                                                                                                                                                                                 sequence.
AL731717
AL731717.10
                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Quality coverage: 15.82 in Q20 bases; agarose-fp
Quality coverage: 9.51 in Q20 bases; sum-of-contigs
Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton
                                                     Brown, J
                                                                                                                                                                                                                                                                                                            Mouse DNA sequence
                               Direct Submission
                                                                                                                                                                                 Mus musculus.
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195027. .291588
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128634. .194926
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/chromosome="UNK"
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/db_xref="taxon:10090"
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54654 c 54286 g 89797 t
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83.9%;
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gap of unknown length
contig of 25342 bp in length
gap of unknown length
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om clone
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                            bp DNA
RP23-92C4
                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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  REFERENCE
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1 GCTGTTGTTACTTTTCTTCTTCTATTCCA 29
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                        22131767
12136098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2002 this sequence version replaced gi:21690011.
                                                                                                         NotI flanking sequences: a tool for of the human genome
                                                                                                                                                             Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S. Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens genomic sequence
NR5-IL22C.
AJ340055
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                                                                                    Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-92C4 is from the RPCI-23 Mouse PAC Library
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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/db_xref="taxon:10090"
/chromosome="X"
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AUTHORS Zabarovsky, E.R.

TITLE Direct Submission
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
FEATURES
Sweden
Location/Qualifiers
/organism="Homo sapiens"
/db xref="texon:9606"
/d
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Run
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Maximum DB seq length: 2000000000
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2: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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Maximum Match 100%
Listing first 45 summaries
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/geneseqn-embl/NA1988.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21.6	22	22	22	22.4	22.4	22.4	22.4	33	Score
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22	22	22	21	22	22	22	22	21	BB
ABA75350	ABA18639	ABA18638	. AAC43567	AAS11614	AAK72230	AAK64813	AAK72229	AAA96850	ID
Human foetal liver	Human nervous syst	 Human nervous syst 	Zea mays DNA fragm	Human genomic DNA	Human immune/haema	Human immune/haema	Human immune/haema	Guide desoxynucleo	Description

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Human cytokine HCC Gene #3945 used to Breast cancer rela Human differential	DNA encoding novel Gene #2134 used to	negative elo	prostate can	reproductive	ovarian and		e fragm	Drosophila melanog	activat	Human cDNA differe	immune/haema	Bacillus lichenifo	brain expres	DNA encoding human	Human nucleosomal	brain expre	W802.	Human musculoskele	Drosophila melanog	Human musculoskele	sequence #293	#7817 for g	bone marrow	expres	for ge	live	for	bone marrow	expre	for
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ALIGNMENTS

RESULT 1 AAA96850

AAA96850 standard; DNA; 33 BP

AAA96850;

19-FEB-2001 (first entry)

Guide desoxynucleotide building block G2

Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; ss.

Synthetic.

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370

29-MAR-1999; 99FR-0003925

(MERI-) MERISTEM THERAPEUTICS.

Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62

Chimeric expression promoter for transgenic plant production, comprises

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RESULT 2
AAK72229/c
D AAK72229 standard; DNA; 569 BP.
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Best Local S
Matches 33
18-APR-2000
19-MAY 2000
07-UUN-2000
28-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
26-JUL-2000
14-AUG-2000
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14-AUG-2000
                                                                                                                                                                                                                                                      31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a guide desoxynucleotide building block, which was used to link directional desoxynucleotide building blocks during construction of chimeric promoters of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematópoietic; immune/haematopoietic cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27041
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2000US-0180628
2000US-0184664
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2000US-0189874
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2000US-0214864
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2000US-0217496
2000US-0220964
2000US-0220964
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Pred. No. 0.016;
Mismatches 0;
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14-AUG-2000;
2000US-0225214

2000US-0225268

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2000US-0225447

2000US-0225475

2000US-0225475

2000US-022548681

2000US-0226279

2000US-0228924

2000US-0228924

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2000US-0235836

2000US-02344786

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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polymucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic complements from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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01-DEC-2000

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14 AUG-2000;

14 AUG-2000;

14 AUG-2000;

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23 AUG-2000;

23 AUG-2000;

01 SEP-2000;

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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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30-JUN-2000;
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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17-NOV-2000;

Nucleic aci useful for metastasis

Disclosure;

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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2000US-0189350

2000US-0199874

2000US-0199123

2000US-0205515

2000US-021647

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2000US-0225268

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81.2%;
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2000US-0241786.
2000US-0241787.
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2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0246476.
2000US-0246477.
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RESULT 4
AAK72230/c
ID AAK722
XX
AC AAK722:
XX
DT 06-NOV
XX
DE Human:

standard; DNA; 47319

ВP

Gape

0

06-NOV-2001 AAK72230; AAK72230

(first entry)

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27042.

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                                                                                                                             CC AAXS4951 to AAX64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and circular treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAX64703 CC cancers and cancer metastases of haematopoietic derived cells. AAX64703 CC cancers from the present invention. AAX63421 to AAX64950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                            Query Match
Best Local S
Matches 26
12933 GCTGATGTCACTTACCTTCTTGTATTCCAACC 12902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                            Sequence 47319 BP; 13708 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 19625; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
                  1 GCTGTTGTTACTTTTCTTCTTCTATTCCAGCC
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                                                              26;
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash
                                                            67.9%; ilarity 81.2%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249217
2000US-0249218
2000US-0249245
2000US-0249245
2000US-0249265
2000US-0249267
2000US-0249297
2000US-0249297
2000US-0249300
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2000US-02511869
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2000US-02511990
2000US-02511990
2000US-02511990
2000US-02511990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben
                                                              0
                                                                                                                            8453 C;
                                                            Score 22.4; D
Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS
                                                                                                                            9720 G; 15438
                              32
                                                                             DB 22, 2e+02;
                                                                                            22;
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                                                                                          Length 47319;
                                                                                                                             7;
0
                                                               Indels
                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides, and
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2	8 2 2 8	ZZZZ
09-AUG-2001. 17-JAN-2001. 13-JAN-2000. 04-FEB-2000. 04-FEB-2000. 16-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-JUL-2000. 20-JUN-2000. 20-JUN-2000. 20-JUN-2000. 11-JUL-2000. 11-AUG-2000. 11-SEP-2000.	Homo sapiens. WO200157182-A2	ı; immu static;
2001WO-US01354. 2000US-0119065 2000US-01180628 2000US-0184664 2000US-0184664 2000US-019076 2000US-0190176 2000US-02151313 2000US-0216647 2000US-0217496 2000US-0217496 2000US-0217496 2000US-0217496 2000US-0217496 2000US-0217496 2000US-0217496 2000US-0217497 2000US-0217497 2000US-0217497 2000US-0217497 2000US-0225214 2000US-0225214 2000US-0225213 2000US-0225214 2000US-0225275 2000US-0225270 2000	A2.	haematopoi ne therapy;
		etic; immune/haematopoietic vaccine; metastasis; ds.
		oietic ds.
		antigen; cancer;
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RESULT 5
AAS11614
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                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequences given in AAM82170 to AAM919121. (I) have cytostastic cativity, and can be used in gene therapy and vaccine production. (I) compression and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) concerns may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic concers from the present inwention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                          12933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                       CRIM-1; Human; human chromosome 2p21-16.3; ophthalmological; neuroprotective; renal; osteopathic; dental; vulnerary; immunogen; antibody; gene therapy; neurodegenerative disease; eye disorder; cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;
  intron
                                 exon
                                                                                             exon
                                                                                                      Key
                                                                                                                          Homo sapiens
                                                                                                                                                                                                          Human genomic DNA containing exons 2-17 of the CRIM1 gene.
                                                                                                                                                                                                                              24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                       AAS11614 standard; DNA; 236303 BP
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47319 BP; 13708 A; 8453 C; 9720 G; 15438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 27042; 3071pp + Sequence Listing; English
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05-JAN-2001; 2001US-0259678.
                                                               intron
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                                                                                                                                                                                                                                                                                                                                      1 GCTGTTGTTACTTTTCTTCTTCTATTCCAGCC 32
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                                                                                                                                               abnormality; wound; ds.
                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                 67.9%;
ilarity 81.2%;
Conservative
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Pred. No. 1.2e+02;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 47319;
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CC and the encoded peptide (and mouse and chicken orthologues) that CC comprises a PGECCPLP group, an insulin-like growth factor binding protein CC (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group CC and a transmembrane domain. The protein, e.g. CRIM1, interacts with CC peptides of the transforming growth factor superfamily. A composition CC comprising an expression construct comprising the nucleic acids of the CC invention or a mimetic which antagonises or mimics an activity of a CRIM1 CC polypeptide may be used in a method for modulating the biological CC activity of a polypeptide of the bone morphogenic protein (BMP) family. CC especially cataract formation. They may also be used to treat an eye disease, CC especially cataract formation. They may also be used to treat CC abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in CC gene therapy by using antibodies directed against CRIM1 polypeptides. CC The present sequence is a Human genomic DNA containing exons 2-17 of CX XX
RESULT 6
AAC43567
ID AAC4
XX AAC4
XX AAC4
XX T17-0
DT 17-0
DE Zea
XX Hybr
KW prot
                                                                                                                                          Db 214710
                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide, useful for preventing, diagnosing and treating e.g. eye disease, especially cataract formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
protein identification; signal transduction pathwa pathway; promoter; termination sequence; corn; ss.
       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic;
                                                                          AAC43567;
                                                                                                                                                                                                                 Sequence 236303 BP; 70199
                                    Zea mays DNA fragment SEQ ID NO: 39699.
                                                       17-OCT-2000
                                                                                            AAC43567
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 3; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Little
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                                                                                                                                                     GCTGTTGTTACTTTTCTTCTTATTCCAGCC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M, Yamada T,
                                                                                                                                                                             26;
                                                                                                                                                                                      Similarity
                                                                                           standard; DNA; 458 BP
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                                                        (first entry)
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81.2%;
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10-JUN-1999
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S-0127462.
S-0128234.
S-0128714.
                                             3-0139763
3-0139817
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3-0136392.
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3-0130510.
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RESULT 7
ABA18638/c
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AC ABA18638
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Best Loc
Matches
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16-SEP 1999
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24-SEP 1999
24-SEP 1999
26-SEP 1999
27-SEP 1999
28-SEP 1999
29-SEP 1999
29-CT 1999
11-OCT 1999
                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatocropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                               neurological
                                                                                                                                                                                                                                                                                 23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
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                                                                                                                                                                                                                                           nervous
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l Similarity 83.3%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                 disease;
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99US-0154779
99US-0155139
99US-0155286
99US-0155286
99US-0155259
99US-0156596
99US-0157533
99US-0159293
99US-0159293
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99US-0159295
99US-0159295
99US-0159295
99US-0159331
99US-0159231
99US-0159231
99US-0160741
                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                        related
                                                                 infection; nephrotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                      polynucleotide SEQ ID
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1.2e+02;
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                                                                 gene
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                                                                 therapy;
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                                                                 vaccine;
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                                                                 8b
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99US-014091 99US-014187 99US-0142154 99US-014220 99US-014220 99US-014297 99US-014427 99US-014427 99US-0144085 99US-0144325 99US-0144331 99US-0144326 99US-0146388 99US-0147204 99US-0147204 99US-0147204 99US-0147204 99US-014731 99US-014931 99US-014931 99US-014931 99US-014931 99US-014931 99US-014931 99US-014931 99US-014931 99US-014931 99US-014933 99US-014933 99US-0151066 99US-0151066 99US-0151303 99US-0151303 99US-0151333 99US-0151333

20-JUL-1999, 20-JUL-1999, 21-JUL-1999, 21-JUL-1999, 21-JUL-1999, 22-JUL-1999,

22-JUL-1999
22-JUL-1999
22-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
26-JUL-1999
27-JUL-1999
28-JUL-1999
28-JUL

sapiens

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WC200159063-A2 16-AUG-2001. 17-JAN-2001. 24-FEB-20000; 22 24-FFB-20000; 22 24-FFB-20000; 22 24-FFB-20000; 22 24-FFB-20000; 22 24-FFB-20000; 22 24-FFB-20000; 22 26-JUN-20000; 22 27-JUN-20000;
#2. 2001WO-US01334. 2000US-0119065. 2000US-0184664. 2000US-0184664. 2000US-0184664. 2000US-0184664. 2000US-0198123. 2000US-0199123. 2000US-0216486. 2000US-0216486. 2000US-0216486. 2000US-0216486. 2000US-0216486. 2000US-0216486. 2000US-0216486. 2000US-0216880. 2000US-0216880. 2000US-0216881. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225277. 2000US-0225779. 2000US-023343. 2000US-0233239. 2000US-02
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CT-2000; 20
2000US -02363 2000US -02370 2000US -02370 2000US -02370 2000US -02370 2000US -02418 2000US -02418 2000US -02418 2000US -02418 2000US -02418 2000US -02464 2000US -02466 20
B B G G G G G G G G G G G G G G G G G G

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RESULT 8
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ID ABA18639
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Best Local S
Matches 25
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 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB16678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmonytic anaemia, autoimmune thyroiditis, diabetes mellitus. Crohn's disease, allergies, autoimmune disorders e.g. Addison's disease, allergies mellitus.
                                                                                                                                                                                                                                                                Human; pootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hapatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13079 BP; 4243 A;
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                                                                                                                                   17-JAN-2001;
                                                                                                                                                                16-AUG-2001.
                                                                                                                                                                                           WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA18639;
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                                                                                                                                                                                                                                                    neurological
                                                                                                                                                                                                                                                                                                                                                                     Human nervous system related polynucleotide SEQ ID NO 10970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
ilarity 83.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastases
 2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
                                                          2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
                                                                                                                                                                                                                                                    disease;
                                                                                                                                   2001WO-US01334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10969; 1701pp +
                                                                                                                                                                                                                                                    infection; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25967
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es 5;
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                                                                                                                                                                                                                                                    therapy; vaccine;
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26-JUL-
14-AUG-
14-AUG-
14-AUG-
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18-AUG-
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                  Nucleic useful f
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) accomises are weared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                       -NOV-2000;
                                                           for preventing, and metastases
                                                                                                                      HUMAN
                                                                                                       Barash
                                             SEQ
                                                                                                                                                                                                                                                 2000US-0249264.
2000US-0249265.
2000US-0249297.
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2000US-0249208.
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2000US-0254097
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2000US-0246477.
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2000US-0246474.
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                                                                                                                      GENOME
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                                                                                                      SC,
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                                                                                                                     SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       246524
246525
                                             10970;
                                                            3224 human
diagnosing
                                                                                                                                                                                                                                                                              49244.
                                           1701pp +
                                                                                                       MS
                                                                  nervous system antigen polypeptides, and/or treating nervous system
                                            Sequence
                                                                 treating
                                           Listing;
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English

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RESULT 9
ABA75350
ID ABA75350
ID ABA75350
ID ABA75350
AC ABA7
XX ABA7
XX Huma
XX Huma
XX Huma
XX Hom
CXX The
CCC Mea
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                                                                                                                                                                                                                                                                                           Human genc
analyzing
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound haaling; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25967 BP; 8245 A; 4194 C;
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                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian cancer and other cancers of the adrenal gland,
                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTTGTTACTTTTCTTCTTCTATTCCAG
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                                                                                                                                                                                                                                                                                              genome-derived single zing gene expression in
                                                                                                                                                                                                                                              4; SEQ ID NO 23655; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 foetal liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                                              in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression; single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                                                                                                                                                                                                              exon nucleic
n human fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4708
                                                                                                                                                                                                                                                                                                                                                                                                                     뮸
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G;
                                                                                                                                                                                                                                                                                              acid p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8820
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                                                                                                                                                                                                                                                                                                                    probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone,
                                                                                                                                                                                                                                                                                                                      for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
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RESULT 10
ABA39992
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                     Query Match
Best Local S
Matches 24
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                    Sequence
                                                                                       Note: The sequence data for this patent did not specification, but was obtained in electronic foat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                         probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease
                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #18458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA39992 standard; DNA; 144 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                           Claim 4; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
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 TGTTGTTACTTTCTTCTTCTATTCCAG 30
                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGTTACTTTTCTTCTATTCCAG 30
                                                                                                                                                                                                                                                                           exon nucleic acid
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24; Conser
                      ! Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                    144
                                                                                                                                                                                                                                                                                                                         Hanzel
                     65.5%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTTTCTTCTTCTCTAG
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                                                                    вp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                         ID No 18458; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                     2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                    27
                                                                                                                                                                                                                                                                                                                        Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                  A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%;
                                                                                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                                                                                            probes
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Pred. No. 1.6e+
0; Mismatches
                      0,
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                     Score 21.6; DB 22
Pred. No. 1.6e+02;
0; Mismatches 4
                                                                  12 G;
                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                             for
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                                                                    72 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                         뮸
                                                                                                                                                                                                                                                                           analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6e+02
                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                    ot form
format
                                          Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                      Indels
                                                                                                   part of the printed directly from WIPO
                     0;
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                                                                                                                                                                                                                                                                            in human
                    Gaps
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                                                                                                                                                system
                     0
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RESULT 12 AAK49980

AAK49980 standard; DNA; 144

ВP

BXAXXXX

AAK49980; 06-NOV-2001

(first entry)

Human bone marrow expressed single exon probe SEQ ID

NO:

24537

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RESULT 11
AAK23906
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                  გ
                                                                                  문
                                          Matches
                                                  Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2
26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
                                                                                                                 brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                  Sequence 144 BP; 27 A; 33 C; 12 G;
                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK23906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK23906
                                                                                                                                                         probes which are derived
                                                                                                                                                                    The present
                                                                                                                                                                                        Example 4; SEQ ID NO: 23897; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157275-A2
                                                                                                                                                                                                                                                                                     (MOLE-)
                                                 Local
29
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            3 TGTTGTTACTTTTCTTCTACTACTACAG 30
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TTTTGTTTCTTTCTTCTTCTTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTGTTTCTTTCTTCTTCTAG
                                          24;
                                                   Similarity
                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed single
                                                                                                                                                                   invention
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                  65.5%;
                                                                                                                                                                    provides a number of single exon nucleic
                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                          from genomic sequences
                                         <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                   Score 21.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon probe
                                          Mismatches
                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
 56
                                                                                  72 T; 0 other;
                                                                                                                                                                                                                                                                  DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:
                                                    .6e+02
                                                              DB 22;
                                                                                                                                                          expressed
                                          Indels
                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23897
                                                              144;
                                                                                                                                                           in the
                                          0
                                          Gaps
                                                                                                                                                samples,
                                                                                                                                                           human
                                                                                                                                                                                                                         human
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RESULT 13
AA127077
ID AA127
XX
AC AA127
XX
DT 12-OC
XX
Probe
XX
Probe
XX
Probe
XX
Cervi
XX
OS Homo
XX
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XX
OS Homo
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               samples, which may enable the such as lymphoma, leukaemia the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone microarray;
                                              30-JAN-2001; 2001WO-US00670
                                                                                                WO200157278-A2
                                                                                                                       Homo sapiens
                                                                                                                                                 cervical
                                                                                                                                                                                  Probe #17010 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                            12-OCT-2001
                                                                                                                                                                                                                                                             AAI27077
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                       TTTTGTTTCTTTTTCTTCTTCTTCTAG
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                                                                                                                                                                                                                                                                                                                                              TGTTGTTACTTTCTTCTTCTATTCCAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                              uman; microarray; gene expression; cervical epithelial cell; cancer; ss.
                                                                                                                                                                                                                                                             standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                        144 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:
; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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2000US-0207456.
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                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        27
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                  65.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24537; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                       Score 21.6; D
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        12
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                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                       Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                  1.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                       0,
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one of
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RESULT 14
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Best Local S
Matches 24
                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207446.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234589.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct semiences
                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                        Penn
                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                      01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression, the probes are therefore useful in grading of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                      30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                ABA62842 standard; DNA; 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                            ABA62842;
                                                            (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from human HeLa cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                     29
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                                       SG
                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTGTTACTTTTTTTTTTTTTCTAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                   2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGTTTCTTTCTTCTTCTTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                 foetal
                                                                                                                                                                                                                                                          foetal liver; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                            MOLECULAR DYNAMICS
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                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                               liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 27 A; 33 C;
                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.5%;
85.7%;
                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to human single exon nucleic acid probequence is one such probe. The SENPs are derived The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                          expression; single
                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.6;
Pred. No. 1
                                        Rank
                                                                                                                                                                                                                                                                                nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     56
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                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                          nucleic acid probe;
                                                                                                                                                                                                                                                                                 #11147.
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88

Human

genome-derived single exon nucleic acid probes useful for

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RESULT 15
ABA30124
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Best Local 9
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, disgnosing, grading, staging, monitoring and prognosing diseases of the human heart.
                                                                                                                                                                                                                                     Single exon
                                                                                                                                                                                                                                                                                    WPI; 2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA30124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA30124 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 568 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                              Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 11147; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                         hearts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  congenital heart
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                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
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                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
                                                                                                                                                                            ID No 8590; 530pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 A; 95 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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85.7%;
                                                                                                                                                                                                                                                                                                                          Chen W,
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                                                                                                                                                                                                                                         probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21.6; In Pred. No. 1.7e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 G;
                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                              English
                                                                                                                                                                                                                                       for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                            뮸
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length
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                                          Matches
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                                                                                                   congenital heart disease.

Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                   Sequence 568 BP; 196
 97
                                                                                                                                                 g. cardiovascular disease,
                     w
TTTTGTTTCTTTCTTCTTCTAG 124
                      TGTTGTTACT
                                         24;
                                                   Similarity
                                         Conservative
                   TTCTTCTTCTATTCCAG 30
                                                   65.5%;
                                                                                  A; 95 C;
                                         0; Mismatches
                                                   Score 21.6;
Pred. No. 1.
                                                                                                                                                hypertension, cardiac
                                                                                   69 G;
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                                                                                   other;
                                          4.
                                                                                                                   format
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                                                                                                                  part of the printed directly from WIPO
                                                              568;
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Search completed: Job time : 108.18 мау : 11, 2003, 03:06:50

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Result
No.
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB seq length: 0
DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May 11, 2003, 02:44:10 ; Search time 13.2331 Seconds (without alignments) 764.775 Million cell updates/sec
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33
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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     US-09-687-477-11
US-09-687-477-13
US-09-687-477-13
US-09-687-477-13
US-09-134-01C-1709
US-09-134-01C-1709
US-08-472-217-3
US-08-474-219B-16
US-09-426-290-1
US-09-434-01C-212
US-09-434-01C-212
US-09-434-01C-212
US-09-134-01C-212
                                                                                                                                                                                                                                                                                                                                   US-08-973-675-1
US-08-687-080-59
US-07-662-005A-15
US-09-002-114-2
US-09-687-477-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
Sequence 69, Appl
Sequence 81, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 1709, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 234, Appl
Sequence 234, Appl
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     Query Match
Best Local Similarity
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61.8%;

Score 20.4; Pred. No. 58;

BB

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RESULT 1
US-09-453-702B-69/c
US-09-453-702B-69/c
; Sequence 69, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; TOPOLOGY: linear MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 69: US-09-453-702B-69
                                                                                  INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                          APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.9501:
                                                                                                                                                                                                                                                                    ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE Diskette, 3.50 inch.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARAE: WOO'D PETFECT 8.0
CURRENT APPLICATION DATA:
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 26173
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 South Pinckney Street CITY: Madison
                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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Plunkett, or,
Rod
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Parma, Nicole T.
                                                                                                           E: (608) 251-50
(608) 251-9166
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US-09-232-149A-234
US-09-280-116-203
US-09-328-111-46
US-08-718-538-4
US-08-719-376-1
US-08-719-35-4
US-09-134-591-4
US-09-134-591-4
US-08-702-525-1-2
US-08-702-525-1-2
US-08-704-476-179
US-08-441-430-31
US-08-441-430-31
US-08-627-2476-29
US-08-627-254C-29
US-08-930-589A-119
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Patent No.

APPLICANT: APPLICANT:

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US-09-302-620B-81/c
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                                                                                       APPLICANT: Gleegon, MATTIN
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
FILE REFERENCE: 1010-16.seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81, Application US/09302620B
                                                        NUMBER OF SEQ ID NOS: 109
SOFTWARE: PATENTY ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 109
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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APPLICANT: Craft, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1207 TGTTTTTATTATTCTTCTTCAATGTCAGCAA 1177
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5. 6331420
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Eshoo, Mark
                                                                                                                                                                                                                                                                  Tang, Maria
                                                                                                                                                                                                                                                  Loper, John C.
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Pred. No. 73;
0; Mismatches
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                                                                                           RESULT 5
US-08-687-080-59
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                                                                                                                                                                                                                                                                                                                        US-08-973-675-1
                   Sequence 59, Applicat:
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregor
                                                                                                                                                                                                                                            Best Local Similarity Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, App110
Patent No. 598528
                                                                                                                                                                                                                                                                               Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                      1562 TTGTCTCTTTCTTCCATTTCAG 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HATEBOER, GUUS
APPLICANT: BERNARDS, RENE
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NO.
                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 22201-4714
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TYPE: nucleic acid
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                                                                      Application US/08687080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2623 base pairs
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150..1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                   cDNA to mRNA
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                                                                                                                                                                                                                                                                59.4%; Score 19.6; 84.6%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/973,675
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Pred. No. 73;
                                                                                                                                                                                                                                                  Mismatches
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SOFTWARE: P

TYPE: DNA

4206

US-09-302-620B-82

SEQ ID NO 82 LENGTH: 4145

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US-07-662-005A-15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 5760 TRACTCTTTTCTTCTGCTCCAGCCA 5785
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
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                                                                                                                                                                                       TITLE OF INVENTION: IMPROVED PROCESSING OF PROTEINS NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                   APPLICANT: Van Dijl, Jan M. APPLICANT: Smith, Hilde E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14855 base pairs
TYPE: nucleic acid
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                                                                                                                            STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
                                                                                                                                                      ADDRESSEE:
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5. 5246838
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                                                                                                           CALIFORNIA
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                                                                                              USA
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Quax, Wilhelmus J.
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PatentIn Release #1.0, Version #1.25
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84.6%;
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Pred. No. 1
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US-09-002-114-2/c
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US-09-002-114-2
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Best Local Similarity 81.5
22; Conservative
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                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MUTABhige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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LENGTH: 1314 base pairs
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                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 31/2
CTTY: Palo Alto
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                      LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Corley, Neil C.
                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herew
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              linear
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Pred. No. 1
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                                                                                                                                 ; TYPE: DNA
; ORGANISM: King Salmon
US-09-687-477-11
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ORGANISM: Chum Salmon
US-09-687-477-7
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Best Local Similarity
Matches 22; Conserv
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SOFTWARE: FBBLSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 594
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 594
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Best Local Similarity
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APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
TITLE OF INVENTION: Fish
                                                                                                                                                                                                                                                  FILE REFERENCE: 2213.1004-000
CURRENT APPLICATION NUMBER: US/09/687,477
CURRENT FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                  APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
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APPLICANT: Harris, H. William, Jr.
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous TITLE OF INVENTION: Fish
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                                                              Conservative
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76.7%;
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Pred. No. 1.3e
0; Mismatches
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Pred. No. 1.3e+02;
0; Mismatches 7;
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Pred. No. 1.2e+02;
0; Mismatches 5
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SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 15; LENGTH: 594; TYPE: DNA; ORGANISM: Sockeye Salmon US-09-687-477-15
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; TYPE: DNA
; ORGANISM: Pink Salmon
US-09-687-477-13
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Sequence 6, Application US/09146053A Patent No. 6399349
GENERAL INFORMATION:
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Sequence 15, App. --
Sequence 15, App. --
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TITLE OF INVENTION: Methods for Raising Pre-Adult
TITLE OF INVENTION: Pibe
FILE REFERENCE: 2213.1004-000
CURRENT APPLICATION NUMBER: US/09/687,477
CURRENT FILING DATE: 2000-10-12
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-10-12
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TITLE OF INVENTION: Fish
FILE REFERENCE: 2213.1004-000
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APPLICANT: AquaBio Product Sciences,
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Nearing, Jacqueline
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Russell, David R.
Nearing, Jacqueline
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76.7%;
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Pred. No. 1
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Pred. No. 1.3e+02;
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APPLICANT: Ryan, James W. APPLICANT: Sprinkle, Terry APPLICANT: Venema, Richard

Joe Curtis C.

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APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 1709
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EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10468 TGACTTTAGTTTTCATCTTCTATCCCTGCC 10439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1191
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                                 CORRESPONDENCE ADDRESS:
                                                    NUMBER OF SEQUENCES:
                                                                        TITLE OF INVENTION: Syndecan Stimulation Of Cellular TITLE OF INVENTION: Differentiation
                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                      Application US/08472217
3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
                                                                                                                                      Lepp , Sirpa
Mali, Markku
                                                                                                          Vihinen, Tapani
W rri, Anni
                                                                                                                                                                               Jaakkola, Panu
Jalkanen, Markku
                                                                                                                                                                                                                   Auvinen, Petri
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Pred. No. 2.4e+02;
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Pred. No. 1.7e+02;
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US-08-760-534A-3
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                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6017727 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08760534A
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 01-DEC-1992
                                          COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JALKANEN, MARKKU
APPLICANT: JAAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                             APPLICANT: VIHINEN, TAPANI
TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                   STATE:
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               APPLICATION NUMBER: US/08/760,534A FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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PRIOR APPLICATION NUMBER: US 08/206,186

FILING DATE: 07-MAR-1994

PRIOR APPLICATION NUMBER: PCT/PF193/00514

FILING DATE: 01-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33.851

REGISTRATION NUMBER: 33.851

REFERENCE/DOCKET NUMBER: 1708.0050004/MAC

TELEPONE: (202) 371-2640

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2196 base pairs
TYPE: NULcleic acid
STRANDEDNESS: double
TOPOLOGY: linear
INCLECULE TYPE: DNA (genomic)

US-08-760-534A-3

Query Match
Best Local Similarity 72.7%; pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps

QUETY MATCH
CONSERVATION TOTAL CONSERVATION

1 GCTGTTGTTACTTTCTTCTTATTCCAGCCA 33

QUETY MATCH
CONSERVATIVE OF MISMATCHES 9; Indels 0; Gaps

QUETY MATCH
CONSERVATIVE OF MISMATCHES 9; Indels 0; Gaps

QUETY MATCH
CONSERVATIVE OF MISMATCHES 9; Indels 0; Gaps

QUETY MATCH
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QUETY MATCH
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB seq length: 2000000000
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      Published_Applications_NA:*

| Cgm2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| Cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| Cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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0 US-09-796-692-5376
0 US-09-796-692-7106
0 US-09-786-92-7106
0 US-09-783-590-151
0 US-09-864-761-8590
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US-10-152-724A-24
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Sequence 16, Appl Sequence 24, Appl Sequence 25312, A Sequence 6086, Ap Sequence 4667, Ap Sequence 4667, Ap Sequence 7106, Ap Sequence 7106, Ap Sequence 7106, Ap Sequence 1510, Ap Sequence 5185, Ap Sequence 5185, Ap Sequence 3181, App Sequence 3181, Ap Sequence 3181, Ap Sequence 3181, App Sequence 3181, App Sequence 3181, Ap Sequence 3181, App Sequence 3181, Ap Sequence 3181, App Sequenc
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;	60.0	60.6	60.6	60.6	60.6	60.6	60.6	60.6	60.6	60.6	60.6	60.6	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.8		63.0	63.0	64.2
ļ	117	5450	5325	5325	4859	4859	1742	1735	599	456	180	180	32203	32203	11879	4037	4037	1301	693	442	442	26173	1251	1251	222	3699
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	US-09-969-373-488	US-10-044-090-504	US-09-764-878-340	US-10-079-854-340	US-09-880-107-1647	US-09-954-456-493	US-09-925-300-33	US-09-070-927A-525	US-09-864-761-13264	US-09-864-761-4507	US-09-864-761-29830	US-09-864-761-21254	US-09-764-869-1849	US-10-091-504-1849	US-09-070-927A-181	US-09-880-107-3942	US-09-954-531-986	US-09-880-107-2134	US-09-925-300-691	US-10-040-862-8072	US-09-796-692-8072	US-10-114-170-69	US-09-764-891-6319	US-09-974-300-264	US-09-864-761-27032	US-09-847-665-6
ļ	488	504	Sequence 340, App	340,	164	493	Sequence 33, Appl	525	13264,	Sequence 4507, Ap	Sequence 29830, A	Sequence 21254, A	Sequence 1849, Ap	Sequence 1849, Ap	Sequence 181, App	Sequence 3942, Ap	Sequence 986, App	Sequence 2134, Ap	Sequence 691, App	Sequence 8072, Ap	Sequence 8072, Ap	Sequence 69, Appl	6319,		Sequence 27032, A	Sequence 6, Appli

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: P99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 16
LEGITH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
PRIOR MATTION: Guide decorption of the content of the co
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US-10-152-724A-24
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US-09-963-803-16
Sequence 24, Application US/10152724A
Publication No. US20030082714A1
GENERAL INFORMATION:
APPLICANT: LITTLE, Melissa
APPLICANT: HOLMES, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 33; Conserva
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Guide desoxynucleotide building OTHER INFORMATION: block G2
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No. US20030028922A1
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Conservative (
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Pred. No.
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APPLICANT: GEORGAS, Kylie
APPLICANT: WILKINSON, Lorine
TITLE OF INVENTION: No. US20030082714A1el Nucleic Acid and Polypept
FILE REFERENCE: P22378
CURRENT APPLICATION NUMBER: US/10/152,724A
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: Australian App No. US20030082714A1PQ 4348
PRIOR PILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Datanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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TYPE: DNA
ORGANISM: Homo sapiens
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 2000-0
                   APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                             FILING DATE:
                                                                              APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                     APPLICATION NUMBER: .PCT/US01/00668
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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                                                                                                     FILING DATE:
                                                                                                                      APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00664
  FILING DATE: 2001-01-30 APPLICATION NUMBER: US
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                                                           2001-01-30
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81.2%;
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60/234,687
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Pred. No. 82
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Best Local S
Matches 24
SEQ ID NO 6086
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No.
                                              SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                       PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/796,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HELAT, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: MT HIT: B8786184.1, EVALUE 1.00e-20
OTHER INFORMATION: NT HIT: g17706668, EVALUE 7.00e-21
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OTHER INFORMATION: MAP TO AL121953.10
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                                                                                                                APPLICATION NUMBER: 60/223,378
                                                                                                                                           APPLICATION NUMBER: 60/223,416 FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/200,779 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/200,545 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/218,950 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/206,201
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/200,999
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                                                                                                                                                                                          FILING DATE: 2000-08-03
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                                                for Windows Version
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Pred. No. 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 014058-013520US
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LOCATION: (308)
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OTHER INFORMATION: n=A,T,C
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OTHER INFORMATION: n=A,T,C
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APPLICATION NUMBER: US 60/200,779
                                                                FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
                                                                                                                   APPLICATION NUMBER: US 60/206,201 FILING DATE: 2000-05-22
                                                                                                                                                                  APPLICATION NUMBER: US 60/202,084
                                                                                                                                                                                                     APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/200,303
                              APPLICATION NUMBER: US 60/223,416
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                                                                                                  NUMBER: US 60/218,950
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Pred. No. 7
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RESULT 6
US-09-796-692-4667/c
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Best Local Similarity
Matches 24; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6086
                                                                                                                                                                                                                                                                                                                                                            Sequence 4667, Application US/09796692
Publication No. US20020198362A1
                                                                                                                CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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PEATURE:
NAME/KEY: unsure
NAME/KEY: (217)
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP-
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                            APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/796,692
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OTHER INFORMATION:
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LOCATION: (213)
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LOCATION: (281)
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                                                                                                  APPLICATION NUMBER: 60/190,479
FILING DATE: 2000-03-17
APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
                              APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/
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Pred. No. 72;
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SEQ ID NO 5376
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TITLE OF INVENTION: CONSISTIONS AND METHODS FOR THE DETECTION, DIAGNOSIS
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077,001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                           PRIOR FILING DATE:
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                     ORGANISM: Homo sapiens
FEATURE:
                                                    TYPE: DNA
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 NAME/KEY: unsure
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FILING DATE: 2000-03-17
APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
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APPLICATION NUMBER: 60/186,126
FILING DATE: 2000-03-01
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FILING DATE: 2000-08-03
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APPLICATION NUMBER: 60/223,378
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FILING DATE: 2000-05-22
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Pred. No. 76;
0; Mismatches
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RESULT 9
US-10-040-862-4667/c
US-10-040-862-4667, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
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RESULT 8
US-09-796-692-7106/c
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; OTHER INFORMATION: n=A,T,C
US-09-796-692-5376
                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-796-692-7106
                                                                                                                                                                   SEQ ID NO 7106
LENGTH: 408
TYPE: DNA
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                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAF
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
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FILLING DATE: 2000-03-17
APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
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APPLICATION NUMBER: 60/186,126
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TTTTGTTTCTTCTTCTCTCTCTAG
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                                                                                                                                                                                                                                                                                                                            LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: 60/200,999
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                                                                               Similarity
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Pred. No. 76;
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US-10-040-862-5376/c
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; ORGANISM: Homo sapiens
US-10-040-862-4667
                                                                                                                                                                                                                                                                                                                                                                         Sequence 5376, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                              APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
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PRIOR FILING DATE: 2000-04-27
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CURRENT FILING DATE: 2001-11-06
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
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APPLICATION NUMBER: US 60/200,779
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NUMBER: US 60/202,084
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NUMBER: US 60/223,378
2000-08-07
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85.7%;
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Pred. No. 76;
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US-10-040-862-7106/c
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; LOCATION: (165)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-5376
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                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap, TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US
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APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
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                                                  APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
                                                                                                                                                                                                                                                        NT FILING DATE: 2001-11-06
APPLICATION NUMBER: US 60/186,126
FILING DATE: 2000-03-01
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FILING DATE: 2000-04-27
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                                                                                                            FILING DATE:
                                                                                                                        APPLICATION NUMBER: US 60/200,779
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. US20030078396A1
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: 2000-04-28
NUMBER: US 60/206,201: 2000-05-22
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Pred. No. 76;
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; ORGANISM: Homo sapiens
US-10-040-862-7106
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US-09-783-590-151/c
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LENGTH: 499
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PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, Willia
APPLICANT: Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen, Craig A. APPLICANT: Ruben, Steven M.
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                                            LOCATION: (344)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (369)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (295)
OTHER INFORMATION: n equals
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LOCATION: (284)
OTHER INFORMATION: n equals
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LOCATION: (10)
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
            OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                   LOCATION: (324)
OTHER INFORMATION: n equals
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FILING DATE: 2000-08-07
APPLICATION NUMBER: US 09/796,692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/222,903
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24; Conserv
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NUMBER: US 60/223,416
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                                                                                                                                                                                                                       a,t,g,
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Pred. No. 76;
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                               PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8590, Application US/09864761 Patent No. US20020048763A1
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Best Local
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
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OTHER INFORMATION: n equals a,t,g,
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                    LING DATE:
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NUMBER: PCT/US01/00664
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Pred. No. 78
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FOR

APPLICATION NUMBER: PCT/US01/00668

2001-01-30 NUMBER: PCT 2001-01-30 NUMBER: PCT 2001-01-30

NUMBER: PCT/US01/00663

APPLICATION NUMBER:

PCT/US01/00665

APPLICATION NUMBER: PCT/US01/00669

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OTHER INFORMATION: EXPRESSED IN BRAIN, SOUTHER INFORMATION: EXPRESSED IN HELA, SOUTHER INFORMATION: EXPRESSED IN ADULT LOTHER INFORMATION: EXPRESSED IN HEART, OTHER INFORMATION: EXPRESSED IN HEART, OTHER INFORMATION: EXPRESSED IN BONE MAD OTHER INFORMATION: EXPRESSED INFO
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Publication No. US20030027139A1
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NUMBER OF SEQ ID NOS: 49117
                                                               TITLE OF INVENTI
                                                                                              APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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   CURRENT FILING DATE:
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R FILING DATE: 2000-06-30
R APPLICATION NUMBER: US 09/774,203
R APPLICATION NUMBER: US 09/774,203
R D C C 2001-01-29
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APPLICATION NUMBER: US/09/822,846 FILING DATE: 2001-03-29
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                                                                                                                                                              Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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LaVallie, Edward R.
Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                  Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                               Clark, Hilary
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Treacy, Maurice
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                                                                                                                                                                                                                                                                                                       Fechtel, Kim
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85.7%;
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IN BONE MARROW, SIGNAL = 1.7
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Pred. No. 80;
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ADULT LIVER, SIGNAL = 1.9
FETAL LIVER, SIGNAL = 1.9
HEART, SIGNAL = 2.4
COLUMN 1 = 2.4
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Search completed: May 11, 2003, 06:28:01 Job time : 36.6692 secs

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                                                                                                                        NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5185
LENGTH: 356
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5185, Application Sequent No. US20020160378A1
                                                          Matches
                                                                                      Query Match
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LENGTH: 1057
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                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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SOFTWARE: PatentIn Ver. 2
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ORGANISM: Homo sapiens
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277 TGTTGTTCTTCTTCTTCTATTACAACAA 307
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Wang, Xun
Zhu, Tong
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REFERENCE AUTHORS

TITLE JOURNAL

1 (bases 1 to 31)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating :
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 17 05-OCT-2000;

from

commelina yellow

VERSION KEYWORDS SOURCE

ORGANISM

synthetic construct.
synthetic construct
artificial sequences.

RESULT 1
AX036751
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AX036751 Sequence AX036751

17

from Patent GI:11226260

31 bp WO0058485.

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ALIGNMENTS

AX036751.1

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ö Score 21.6 22 % Query Match 147570 151514 Length 140855 124040 159702 191453 106755 189999 156159 186932 169069 87780 194106 밁 AC016287 AC068437 AC006497 AC006714 AC113061 AL831778 AC120343 AL354883 AC107678 AC101950 AC11 AC092756 Ħ AP003896 AC107585 AC010029 AC097412 AP003896 AC108151 Homo sapi AC006497 Drosophil AC006714 Caenorhab AC113061 Mus muscu AL831778 Mus muscu Z50038 D.virilis D Description Caenorhabdi Rattus no Drosophil Drosophil Z Rattus no 6 Oryza sat Drosophil 2 Homo sapi 4 Homo sapi 4 Rattus no Homo sa Homo sa Rattus Homo Homo Human DNA Rattus no Mus muscu Oryza sat Human DNA Mus muscu Mesorhizo Homo sapi Homo sapi Homo sapi Rattus no Mus muscu Sequence Rattus no Mus muscu Rattus no Mus muscu Mus muscu Mus muscu muscu sapi sapi sapi sapi sapi

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              Alborooks, S. L., Amaratunge, H. C., AFE, J. K., Ayele, M., Banke, T., Barbarta, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bryd, N.C., Burrell, K.L., Byyd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Dealaney, K.R., Delgado, O., Denin, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Drayer, H., Dugan-Rocha, S., Durbin, K.J., Dealaney, K.R., Delgado, O., Denin, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Drayer, H., Dugan-Rocha, S., Durbin, K.J., Dealaney, K., Rarcia, A., Garner, T., Garza, M., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, D., Lichtergo, K., Hartin, K., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Lewis, L. Kratovic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Lewis, L. Li, J., Li, Z., Lichtergo, O., Lieu, G., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Mayue, P., Martin, R., Martinala, A., Martinez, B., Massey, E., Mawhiney, B., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Mguyen, N., Nickerson, S., McKetshwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Sonaike, T., Sparka, A., Stanley, H., Stone, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, S., Walken, M., Martinez, S., Swery, G., Sonaike, T., Sparka, A., Stanley, H., Stone, H., Stone, H., Stone, H., Wall, S., Marton, R., Wang, Q., Wu, Y., W., Z., Zhou, J., Zorrilla, S., Nelson, S., Worley, K., Martinez, S., Sept, M., Rojas, A., Rojas, A., Rojas, A.,
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4, *** SEQUENCING IN PROGRESS
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Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 107637 bases at least Q40
Consensus quality: 112100 bases at least Q30
Consensus quality: 114998 bases at least Q20
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9963792
                                                                                                                           Submitted (01-MAR-2002) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, On Aug 31, 2001 this sequence version replaced (
                                                                                                                                                                                                                                                                                                                                                        Submitted (31-AUG-2001) Genome University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                      University, 4444 Forest 6 (bases 1 to 170897)
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                                                                                                              ----- Genome Center
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                 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: H_NH0472L21
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piens BAC clone
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dicine, 4444 Forest Park Parkway, St.
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, Missouri 63108,
gi:14030137.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction This sequence was finished as follows unless otherwise noted: digest.

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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Freng Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.r. Genomics 51:1-8. The clone may be obtained either from enetics, Inc. (http://www.resgen.com) or Pieter de Jong Frengen, E

NEIGHBORING SEQUENCE INFORMATION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-472L21"
/clone_lib="RPCI-11"
1034.__2872
                                                                                                                        rpt_family="AT_rich" 6018. .16204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
| db_xref="taxon:9606"
| chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST AW969647 (NID:g8159491)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST AI445609 (NID:g4289409) tj08a01.x1"
959. 4218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="(GAAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="(A)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="Alu"
_family="MER1_type"
                                                                                                                                                                                                                                                                                                                                                   family="AT_rich"
. .11595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="Alu"
                                          family="MIR"
                                                                                                                                                                                              family="MaLR"
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                                                                                 family="L2"
                                                                                                           family="MIR"
                                                                                                                                                                   family="Alu"
                                                                                                                                                                                                                          family="L2"
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                                                                                                                                                                                                                                                                                 family="MIR"
                                                                                                                                                                                                                                                                                                         family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                            family="GA-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                         family="ERVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 6565
                                                                                                                                                                              RESULT 4
AC101918
LOCUS
DEFINITION
                                       REFERENCE
AUTHORS
                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
                                                                                                                                                                                                                                                                 Db 38430
                                                                                                                                                      ACCESSION
                          TITLE
                                                                                                                                                                                                                                                                                                                       Query Match 71.0%;
Best Local Similarity 83.3%;
Matches 25; Conservative
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                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 18665) Birren,B., Nusbaum,C. and Lander,E. Mus musculus, Clone RP24-49513 Unpublished
                                                                                                                                                                   AC101918 186665 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP24-49513, WORKING DRAFT SEQUENCE, 20 unordered
pieces.
                                                                                              Mus musculus
                                                                                                       AC101918.2 GI:22381410
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
house mouse.
                                                                                                                                                      AC101918
(bases 1 to 186665)
                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MIR"
26616. .26689
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17237. .17319
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="
25436. .25512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MER2_type"
23851. .23871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L2"
23067. .23213
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MaLR"
25356. .25413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
24405. .25001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER1_type"
24127. .24173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_fami
23216. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="MER1_type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MIR"
1770. .21891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="AT_rich"
9324. .19449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
.8629. .18670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pt_family="MaLR"
|619. .23850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="(TTTTTA)n"
1892. .22185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pt_family="MIR"
[889. .21908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="(CATA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 22538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .20081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .23310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lly="MER1_type"
                                                                                                                                                                                                                                                                                                                       Score 22; DB 9;
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     (TTATA) n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Vence, C., Jamer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travere,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wi,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Aug 21, 2002 this sequence version replaced gi:17060694. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardyna,S., Gord,S., Graham,L., Grand-Pier
Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Karatas,A., Kells,C., Landers,T., Levine,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Bouk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larnoun, J., Zembek, L., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Mathews,C., MacCarthy,M., McEwan,F., McKernan,K., McPheeters,R., Meldrim,J., McCarthy,M., McMarquis, McCarthy,M., McCart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones, C.
NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces
                                                                                                                                                                                                                                  Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 180378 bases at least Q40 Consensus quality: 183287 bases at least Q30 Consensus quality: 184280 bases at least Q30 Consensus quality: 184280 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web
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                                                                                                          Quality coverage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                          Insert size: 188000; agarose-fp Insert size: 184765; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Heaford, A.
                                                                                                      lity coverage: 6.6 in Q20 bases;
lity coverage: 6.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linton, L., Nusbaum, C., Lander, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mihova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to 186665)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barna, N., Bastien, V., Bogustavkıy, J., Chazaro, B., marata, J., Campopiano, A., Chang, J., Chazaro, B., collymore, A., Cook, A. Collangelo, M., Collins, S., Collymore, A., Cook, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkiy,L., Bouxusgarue,B., Choepel,Y., Collymore,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grand-Pierre, N., Hagos, B., Johnson, R., Jones, C., Kamat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boguslavkiy, L., Boukhgalter, B.,
                                                                                                      sum-of-contigs
                                                                                                                                      agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ali,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindblad-Toh, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boukhgalter, B.,
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12204. .16361
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6162: cor
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50393: cont
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6. .30730
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143060: cont
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3423: con
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2119: con
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77181: contig of
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22485: con
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as soon as it is available and the accession number will be preserved.
                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                             is not known and their order in this sequence record
1081: contig of 1081 bp in length
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186665: contig of 43505 12103: contig of 2096 103: gap of 100 by 16361: contig of 4158 p of 100 bp contig of 10117 bp in length contig of 9346 contig of 6024 ap of 100 bp contig of 16417 bp in contig of 14821 bp in contig of 8145 contig of 1329 bp in length contig of 938 tig of 20829 of 1353 bp 100 100 100 100 100 100 100 100 100 bp 100 100 bp 100 bp dq 001 100 bp 100 bp 100 bp 13412 bp 100 bp 13875 bp 12713 bp in 1186 bp in length 1204 bp 2216 bp å ğ bp in length ģ bp in length đđ ģ ģ å in length Ħ in in length in length length length length

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REFERENCE
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KEYWORDS
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198905 bases at least Q40
                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-WAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 25, 2002 this sequence version replaced gi:20986680.
                                                                                              Sequencing vector: M13; 0%
                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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3 (Dases 1 to 201646)
McPherson,J.D. and Waterston,R.H.
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McPherson, J.D. and Waterston, R.H.
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McPherson, J.D. and Wat
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201646 bp DNA linear HTG 25-
MUS musculus chromosome UNK clone RP23-295K3, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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143161. .186665
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105715. .122131
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Pred. No. 83;
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Query Match 71.0%;
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                                                                                                                                                                ATTGCAGCGTTTACATTCCTGCCTTTCAAT 55839
140855 bp 1
Rattus norvegicus clone CH230-3J16,
78 unordered pieces.
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Insert size: 201820; sum-of-contigs
Quality coverage: 14.37 in Q20 bases; agarose-fp
Quality coverage: 12.44 in Q20 bases; sum-of-contigs
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7068
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201545. .201646
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/note="assembly_name:Contig27"
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50541. .85658
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15059. .24941
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/db_xref="taxon:10090"
/chromosome="UNK"
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50440: contig of 14231 bp in length
50540: gap of unknown length
85558: contig of 35118 bp in length
85758: gap of unknown length
145395: contig of 59637 bp in length
145395: gap of unknown length
201444: contig of 59593 bp in length
201544: gap of unknown length
201646: contig of 102 bp in length
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24941: contig of 9883 bp in length
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7067: gap of unknown length
14958: contig of 7891 bp in length
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                                                                                                                                                                                                                                                                                      Baylor
On Jul
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
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                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2002) Human Genome Sequencing Center, Departed Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

3 (bases 1 to 140855)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                             Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: Project Information
Center project name: GAKM
Center clone name: CH230-3J16
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 78 contigs. The true order of the pieces is not known and their order in this sequence record is
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE0.
                                                                house mouse.
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8487: gap
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5820:
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8: gap of 100 bp
4117: contig of 749
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                                            contig of 756 b p of 100 bp contig of 764 b p p of 100 bp
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Anderson, S., Barna, N., Bastein, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
Gallgan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, L.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schipback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Schipback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wilson, B., Wilson, D., Ye, W. J.,
Direct Submission
M., Shirahand Tnarithe, Mit Center for Genome
Submitted (17-JUN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 71489)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Barra,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Anderson,S., Barna,N., Bastien,V., Tommoniano,A., Chang,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C. and Lander, Mus musculus, clone RP23-137I13 Unpublished
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu - Genome Center

Contact: sequence submissions@genome.wi.mit.edu

Center project name: L26859 Center clone name: 137_I_13

* NOTE: This record contains 85 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will 757: contig of 757 bp in length
758 857: gap of 100 bp
858 1599: contig of 742 bp in length
1600 1699: gap of 100 bp
1700 2430: contig of 731 bp in length
2431 2530: gap of 100 bp
2531 3268: contig of 738 bp (- 3369)
3369

contig

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9329: gap 10077: 10177: gap

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33: contig of gap of

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11854: 11033:

54: gap of 12598: contig of 98: gap of

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18594: gap of 19338: contig of

753: gap or 18494: contig of 18494: qap of 1

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138: gap of 20169: contig of 269: gap of

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                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 120953)
Birren,B., Nusbaum,C. and Lander,B.
Mus musculus, clone RP24-313G10
2 (bases 1 to 120953)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                                                              Mus musculus
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58115: contig
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53955: contig of 7
4055: gap of 10
54768: contig of 7
4868: gap of 11
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44650: contig of 1
4750: gap of 10
45497: contig of 7
5597: gap of 10
46366: contig of 7
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43845: cont
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48885: contig
985: gap of
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41269: c
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52299: contig of
399: gap of 1
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051: contig of
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RP24-313G10,
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38 3237: gap of 38 32893: contig of 756 b 100 bg 194 32993: gap of 100 bg 100 bg 100 bg 100 bg 100 bg

32037:

100 bp of 753 bp

contig p of

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17 28627: contig of 681 bp in 18 28727: gap of 100 bp in 18 29469: contig of 742 bp in 192569: gap of 100 bp in 192569: gap of 192569: g

7 26146: contig of 740 b 7 26246: gap of 100 bp 7 26299: contig of 743 b 7 27089: gap of 100 bp 0 27089: gap of 575 b 0 27846: contig of 757 b

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25406:

2445. 1555: gap of 25306: contig of 751 bp 11. 25306: contig of 750 bp in 1

23699: gap of 24455: contig 22834: gap 23599: c

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22734:

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37065:

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38 37987: gap of 4735 b
88 38722: contig of 735 b
88 38722: gap of 100 bg
23 38822: gap of 100 bg
123 39561: contig of 739 b
123 39661: gap of 100 bg

100 bp f 735 bp

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E 3 (bases 1 to 120953)

S Sirren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarate, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Smith, C., Spencer, B., Stange-Thonann, N., Stojanovic, N., Talamas, J.,
Teefaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 20, 2002 this sequence version replaced gi:17061012. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 12041 bases at least Q30
Consensus quality: 120487 bases at least Q30
Consensus quality: 120534 bases at least Q20
Insert size: 115000; agarose-fp
Insert size: 120653; sum-of-contigs
Quality coverage: 11.1 in Q20 bases; sum-of-contigs
Quality coverage: 10.6 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L20056
Center clone name: 313_G_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site: http://www-seq.wi.mit.edu
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A., Horton,L., Hulme,W., Iliev,I., Jo
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                                                                                                                                                                                                                      sum-of-contigs
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CE 2 (bases 1 to 194106)

RS Birren, B., Linton, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Michova, T., Maenga, V., Murphy, T., Naylor, J., Marquis, N., Mihova, T., Menga, V., Murphy, T., Naylor, J., Mylor, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 194106)
Birren,B., Linton,L., Nusbaum,C.
Mus musculus, clone RP24-494H11
Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36211 a
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15362 73016: contig of 57655 bp in length
73017 73116: gap of 100 bp
73117 120953: contig of 47837 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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clone_end:T7
vector_side:right"
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/clone="RP24-313G10"
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NCE, 14 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research, 320 Charles Street, Cambridge, MA 02141, US All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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1 1278: contig of 1278 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is believed to be correct as given, however the sizes of the gaps between them are based on estimates that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 14 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces % \left\{ 1\right\} =\left\{ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 188000; agarose-fp
Insert size: 192806; sum-of-contigs
Quality coverage: 6.0 in Q20 bases; agarose-fp
Quality coverage: 5.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; n/a; 100% of read Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 189377 bases at least Q30 Consensus quality: 191287 bases at least Q30 Consensus quality: 192278 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                     103033 103132: gap of 100 bp
103133 127989: contig of 24857 k
127990 128089: gap of 100 bp
128990 155768: contig of 27679 k
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                                                                                             organism="Mus musculus"
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7 8586: gap of 100 bp
1 12856: contig of 4270 bp in length
7 12956: gap of 100 bp
7 12956: contig of 9107 bp in length
1 22063: contig of 9107 bp in length
1 22163: gap of 100 bp
/clone_lib="RPCI-24 Male Mouse
                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                   Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (B-mail:kaneko@kazusa.or.jp, URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesorhizobium loti (strain:MAFF303099)
Mesorhizobium loti
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AP002995 BA000012
AP002995.2 GI:14021442
                                      On May 11, 2001 this sequence version replaced gi:11994963.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Takeuchi,C., Yamada,M. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto
Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T.,
Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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155869. .194106
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128090. .155768
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                               ELYDYGEGGFFSFST"
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/translation="MKPHVRAAVAAIALSHSSGRNVSSVYSYSELKYVNIDASVQGNV
VDAYDYNNSCHIDGTLPSLYHYGQNSHIDLQPQSGGQYDGYDYGSNSHFELTVSGNSA
                                                                                                                                                                                                                                                                                                                       /gene="mlr0480" 3429. .3782
                                                                                                                                                                                                                                                                                                                                                                                                                      /prodeit="succinoglycan biosynthesis protein; ExoI"
/protein_id="BAS48058.1"
/protein_id="BAS48058.1"
/db_xref="GI:14021446"
/translation="MPLRLVLVTVAAASALATQFVMHNGGSLPEINLQNLIKPKPVAI
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SGVASVIDGDTIEMHGQRVRFNGIDAESSAVAMVEHGQALDMFKYSNGAYAAQQAKAKA
KPVQCAFVTMATQAFATAGAAMAVEHGQALDMFKYSNGAYAAQQAKAKA
AKVGLMIGSFQAPMDWRAQHSDDAQTPTAPLFATGNGNPGCNIKGNISASGERIYHLP
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KNLVETICRSPDSFISQAAWQAAIRRRPGMVLIHYNSRHVMEKIITPGEPKVPPPQTIV
DGSVHAGQDVALGDLREWHKLRAWCKNCSHHAEVKPAALIKRYGEAALFSTVERALFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1118. .1657)
/gene="mll0476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MYDQTQTTGITAL PYTVVRIRAGDVANPQAVHKGTGFFYHFREG
AGNVPLIVSNKHVLVGKEWLEBPALLLNQKFKFGPANTFRLTKNQLDIFFEHDDTV
DLAAIPIQFIVEAMRGQKEIFNLLLGRETIAFDNIQAILHAATSVLMVDEFFEGNIDE
KNNLPVVRRGILAVNYLTDYRGETNFVVDIAAFGGSSGSPVFAFFENMLPDGSGGVTM
KNLPVYFLGVLHSGPSMTATGKIVPVPVPTSDQIAQTQMMLHLGYCVKASRVEELVE
                                                                                                                                                                                                                                                                                                                                                                                                 GQKYYAVTVISQNKGERWFCSEAEAVAAGWRRSKR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="mlr0479"
2651. .3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein id="BAB48057.1"
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/translation="MALALGGALMKWRLYFVVMTLAVTSGCAADYLNNYDTVTLASGD
ANHTNSLLQTVDPFNPNSNNTHIEGDGQRIVGVVQRYRSPISAGGGYSGNCPTDNSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIRAKISEPTASG"
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/db_xref="taxon:381"
                                                                                                                                                                                                                                                                    notes "unknown protein"
                                                                                                                                                                                                                                                                                            gene="mlr0480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADGSHCGKRSAESRPGGAM"
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/transI_table=
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GIGRAWISSYLVRYLRGYVAAGIDIQEMLDGTFNGRLSKKLLAVVDEAKAGMQGYGRW
SHSEKLKSMINPEMRRINEKHGLEFVEMNCCRWLFFSNNWDALFPDASDRRFNVVANP
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DLDNLLAAFRDEWPGPLAERSDVINYLHVSIAKLFGEKTINKLIEQAGMKLVERISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AITRMPPNAAWELSOSGEGIHIFGRCDKVALGGFRNKWAGWCEPYRTKRFVAFGPGGI
(GRIIOI DWTWOLALILVPARGVGEQDASGEAVERDPRWIGEDEELLERFLASTGGTK
RKLOASPTHLOLWEBHADALAQYFESATGKFPEHSSADQALANVLAFWTGRDYGRIIG
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PYRLPDGSQSLVEVWSEHLAYLIPIEAERVRFEQWLAHIVQRPEELPQSAYLFITEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (7133. 7753)
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                                                                                                                                                                                                                                                                                            complement (10162. .10392)
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/transl_table=
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/gene="mll0483"
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|transl_table=11
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JOURNAL REFERENCE
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ORGANISM
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       TITLE
JOURNAL
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                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Randerson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Canppolano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Perestor, J., Perreira, P., PitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Liev, C., Liu, G., Locke, K., Macdonald, P., Waryuis, N., McCarthy, M., Klein, J., Lunders, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Maryuis, N., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, P., Roy, A., Santos, R., Schauer, S., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Wilson, B., Wilson, B.,
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Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
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1 (bases 1 to 156159)
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156159 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 15 clone RP11-356M20 map 15, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                            Direct Submission
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HFSAMPYPEIPAFAQSIAEREDYSTKALQPLILTATRTNETLGAEWSEIDTEKAVWTI
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L2686. .13279
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Pred. No. 1.5e+02;
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Sequencing vector: M13; M77815; 71% of reads
Sequencing vector: Plasmid; n/a; 29% of reads
Chemistry: Dye-terminator Blg Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 149772 bases at least Q30
Consensus quality: 15233 bases at least Q30
Consensus quality: 153705 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 157000; agarose-fp
Quality coverage: 6.4 in Q20 bases; agarose-fp
Quality coverage: 6.5 in Q20 b

* NOTE: This is a 'working draft' sequence. It currently
consists of 15 contigs. The true order of the pieces
is not known and their order in this sequence record as
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 356_M_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                     128652 128751; gap of 100 bp
128752 153403; contig of 24652 bp in length
153404 153503; gap of 100 bp
                                                                                                                                                                                                                                                                                           101995 102094: gap of 100 bp
102095 128651: contig of 26557 bp in length
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                                                                                                                                                                    ocation/Qualifiers
clone_lib="RPCI-11 Human Male BAC"
                                                                                                                         organism="Homo sapiens"
                         clone="RP11-356M20"
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592: gap of 100 bp
69609: contin of 100 bp
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75994: contig of 6285 k
094: gap of 100 bp
82300: contig of 6206 k
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18619: contig of 2217
719: gap of 100 bg
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Best Local Similarity
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                                  AUTHORS
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                                                                  Direct Submission
Submitted (01-AUG-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                               Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15753)
1 (bases 1 to 15753)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.
            3 (bases 1 to 157533)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
                                                                                                                                                                                                                         Sequencing of human chromosome 15 D15S146-D15S117
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and Hood, L.
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91316. .101994
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9983. .11301
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|2716. .16302
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                                                                                                                                                                                                                                                                                                                                                     sequence.
AC092756
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                                    2 (bases 1 to 189999)
Rowen, L., Madan, A., Qin, S., Baradarani, L.,
Burke, J., Dors, M., Fleetwood, P., Kaur, A., N
Pate, D. and Hood, L.
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 18999)
Submitted (26-JUL-2001) Multimegabase Sequencing Center, Institute
                                                                                                                                   Sequencing of human chromosome
                                                                                                                                                                     Rowen, L., Madan, A., Qin, S., Barac
Burke, J., Dors, M., Fleetwood, P.,
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                                                                                                                                                         Pate,D. and Hood,L.
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Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: leerowen@systemsbiology.org
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Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; ilarity 88.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Data from overlapping BACs AC092756 [drafting center: and AC091748 [drafting center: UMMSC] were added fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="overlap with RP11-429D19 AC092756"
28322. .157533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI human BAC library 11"
/note="Data from overlapping BACs RP11-429D19 and
RP11-99L18 were added and the consensus sequence v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="overlap with RP11-99L18 AC091748"
147556. .147559
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34917 c 33839 g 4346
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/chromosome="15"
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Pred. No. 1.8e+02;
0; Mismatches 3
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He 15 clone RP11-429D19 map 15q21.3,
                                                                                                                                                                         Baradarani,L., Birditt,B., Bloom,S.,d,P., Kaur,A., Madan,A., Nesbitt,R.,
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                                                          Madan, A.,
                                                      Birditt,B., Bloom,S. wadan,A., Nesbitt,R.,
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RESULT 14
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Best Local
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  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Burke, J., Dore, M., Fleetwood, P., Kaur, A., Madan, A., Nes Pate, D. and Hood, L.
  Mclay,K.
                  Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukharyota; Eutheria; Primates;
1 (bases 1 to 106755)
                                                                                                                                                                      AL138779 106755 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 1 clone RP6-65F20 map p32.2-34.1, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98105, USA
On Jan 19, 2002 this sequence version replaced gi:15021994
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Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: leerowen@systemsbiology.org
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                                                                                                               HTGS_PHASE1; HTGS_CANCELLED
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165270. .189999
/note="overlap with RP11-356M20"
41117 c 41361 g 53493 t
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/db_xref="taxon:9606"
/chromosome="15"
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Pred. No. 1.8e+02;
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                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 189999;
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                98963 99062: gap of 1
99063 106755: contig of
                                                                       89256 9299
92959 93058:
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2283 11274: contig of
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98962: con
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 14% of reads
Chemistry: Dye-terminator ET-amersham; 85% of reads
quality: 96644 bases at least Q40
Consensus quality: 99005 bases at least Q30
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On Aug 27, 2000 this sequence version replaced gi:9926429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 104855; sum-of-contigs
Insert size: 117633; 9.0% error; agarose-fp
Quality coverage: 3.06x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the concrys are arbitrary the gaps are unknown runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence this record will be updated with the accession number will be updated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                            69452 69551: gap of 100 bp
69552 73006: contig of 3455 l
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21707 26686; contig of 4980
26687 26786; gap of 100 bp
26787 31996; contig of 527 bp
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49662 52981: contig of 320 b
52982 53081: gap of 100 bp
52982 53082 62347: contig of 9266 b
                                                                                                                                                                                                   77114: contig of 4008 bp 7214: gap of 100 bp 80477: contig of 3263 bp 2577: qap of
                                                                                                                            577: gap of 100 bp
85312: contig of 4735 l
112: gap of 100 bp
89155: contig of 3743 l
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66552: contig of 4105 bp
552: gap of 100 bp
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21606: contig of 4365 bp in length
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2: gap of. 100 bp
11274: contig of 8992 bp in length
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61: contig of 13856 bp in length
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source

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BASE COUNT
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Query Match
Best Local Similarity
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66653. .6945)
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77215. .80477
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73107. .77114
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11375. .17141
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/db_xref="taxon:9606"
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                                                                                                              /note="assembly_fragment:00019
fragment_chain:6
                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00828"
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fragment_chain:5"
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fragment_chain:5"
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fragment_chain:3" ;
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fragment_chain:1"
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ragment_chain:6"
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fragment_chain:6"
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fragment_chain:2"
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Direct Submission

AL Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                       (bases 1 to 129121)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Mellarim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Melarim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, M., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vale, R., Willey, M., Wassiliev, H., Milley, M., Martin, R., Walley, M., Vassiliev, H., Milley, H., X., Warsen, D., Vonne, G., Zainon, I.
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Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:20503130. All repeats were identified using RepeatMasker:
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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                                                                                                                                                                                                           Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
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Birren,B., Nusbaum,C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 182000; agarose-fp
Insert size: 128221; sum-of-contigs
Quality coverage: 7.2 in Q20 bases; agarose-fp
Quality coverage: 10.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.960731
Consensus quality: 126860 bases at least Q40
Consensus quality: 127509 bases at least Q30
Consensus quality: 127930 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the finished sequence as soon as it is available and accession number will be preserved.

alta: contig of 1147 bp in length

1148 1247: gap of 100 bp

1248 2769: contig of 1522 bp in length
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2870 5607: cor
                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-149H21"
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8 BASE COUNT ORIGIN Db 46410 TCCACCTTTTCCTTCCACCCTTTCAATG 46382 Query Match Best Local S Matches 24 misc_feature 3 TCCACCTTTTACATTCCCGCCTTTCATTG 31 Similarity 34269 a Conservative vector_side:right" 1 28590 c 29000 g 36358 t /note="assembly_fragment clone_end:T7 /note="assembly_fragment" 67.7**%**; 82.8**%**; 0; Mismatches Score 21; DB 2; Pred. No. 2.2e+02; Length 129121; 904 others Indels ٥. Gaps

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ALIGNMENTS

GSS 03-JUN-1999

REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CNS00LE5/c LOCUS ACCESSION DEFINITION - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 996) CNS00LE5 996 bp DNA linear GSS 03-JUN-1: Drosophila melanogaster genome survey sequence T7 end of BAC: BACR30A08 of RPCI-98 library from Drosophila melanogaster (fruit Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr Genoscope. Drosophila melanogaster. AL068002.1 fly), genomic survey sequence. AL068002 Direct Submission GI:4958334

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                                        26; Conservative
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL http://image.lln1.gov plate: LLAM10392 row: o column: 24 High quality sequence stop: 423.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                 /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4510703"
/clone=lib="NHH MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
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full-length clones and constructed by Life Technologies.
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/db_xref="taxon:7227"
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Department of Bikaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhaoætigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 400 row: H column: 14
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                       CTGTTGTTACTTTTTTTCTTCTATTCCA 29
                                                                BF397893 479 bp mRNA
UI-R-BS2-bec-h-04-0-UI.sl UI-R-BS2 Rattus
UI-R-BS2-bec-h-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_GSSs: RPCI-24-400H14.TJ
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                                                  BF397893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)
                                BF397893.1
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20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="RPCI-24-400H14"
/clone=lb="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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e RPCI-24-400H14
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                                                                                                                                                                                                                                                                                                                                                                                 TGTTGTTACTTTCTTCTATTCCAGCCA 33
                                   rus musculus (strain:C57BL/6J) adult male testis cDNA to clone lib:RIKEN full-length enriched mouse cDNA library clone:1700011N24.
                                                                                                                                               protein,
AK005882
                                                                                 AK005882.1 GI:12838694
HTC; CAP trapper.
Mus musculus (strain:C5
                                                                                                                                                                                     AK005882 1522 bp mRNA linear HTC Mus musculus adult male testis cDNA, RIKEN full-length library, clone:1700011N24:Retroviral aspartyl protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Scares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
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                                                                                                                                                                 full insert sequence.
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TAG_SEQ=AATCC"
1 92 c 108 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site at ratest.eng.uiowa.edu. The previously described in (Bonaldo, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco RI; The UI-R-BS2 library is a subtracted library derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB=UI-R-BS2
TAG_TISSUE=embry
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/lab_host="DH10B_(Life_Technologies)"
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/db_xref="taxon:10116"
/clone="UI-R-BS2-bec-h-04-0-UI"
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Rodentia;
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Pred. No. 6.9e+03;
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Sciurognathi;
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RS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Adachi,J., Aizawa,K., Bono,H., Brownstein,M., Bult,C., Arakawa,T., Baldarelli,R., Bono,H., Y., Furuno,M., Hanagaki,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hori,Y., Itawa,M., Hiraoka,T., Hori,F., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Myyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Ohido,T., Owa,C., Quackenbush,J., Salto,H., Salto,R., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,D., Sogabe,Y., Suzuki,H., Tagami,M., Tagama,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagama,A., Takahashi,F., Tanaka,T., Yejima,Y., Yoshida,K., Yoshino,M., Muramatsu,M. and
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Yokohama,

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Triticum.
                                                                                                                         sequence.
BQ247773
                                                                                                                                                        BQ247773 634 bp mF TaE25042G03F TaE25 Triticum aestivum
                                                                                                            BQ247773.1
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                                                                              bread wheat.
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Similarity 83.9%;
26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
/clone_lib="AIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
183._.1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPGTSSSRHPHQHQHHYHHHQRIPSTQQAHGLASGENMTFAQELDSPALIRSMLLSNP
HDLSLLKERNPALAEALLSGNLETFSQVIAMEQQRERTLREQBHRELYSTMPPDQBTQA
RIEBERIRQQNIEBENMGIAMEEAPESFGQVAMLYINCKVNGHPLKAFUJSGAQMTIMSQ
ACAERCNIMRLVDRRWGGVAKGVGTQRIMGRVHLAQIQIEGDFLQCSFSILEEQPMDI
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364 c 371 g
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1502. .1507
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/db_xref="GI:12838695"
/db_xref="WGI:12838695"
/db_xref="WGI:1919079"
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/translation="MLITVYCVRRDLTEVTFSLQVNVGLRTPGRTPNHPRADFTGSGSA
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lata source:Pfam, source key:PF00077, evidence:ISS
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clone="1700011N24"
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                                                                                                            GI:20443649
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Pred. No. 4.9e+03;
D; Mismatches 5;
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                                                                                                                                                                        mRNA
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                                                                                                                                                                                                                                                                                                                                               Length 1522;
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BQ249531
BQ249531.1
                                                                                                                                           Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
                                                                                                                                                                                                                                            Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Triticum.
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Contact: Dr. Sylvie Cloutier
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195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                     Plate: 042 row: G colo
Seq primer: M13 Reverse
                                                                                                          Average insert size is >870 Plate: 042 row: G column:
                                                                                                                                                                                                                            Tel: (204) 983-2340
Fax: (204) 983-4604
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(204) 983-4604
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/lab_host="E. coli DH10B"
/note="Vector: pCWV-SPORT6.0 (invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat secof cultivar Glentea 25 days post-anthesis"
136 c 92 g 237 t
                                         Location/Qualifiers
1. .697
/organism="Triticum aestivum"
/cultivar="Glenlea"
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| Cultivar="Glenlea"
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No. 8e+03;
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RESULT 9
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601488248F1 NIH_MGC_69
mRNA sequence.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates;
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nilarity 86.2%;
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                                                                                                                                                                                                                     /clone="IMAGE:3890914"
/clone_lib="NIH_MGC_69"
/tissue_type="large_cell_carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pcMy-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.1 kb. Library constructed by Li
Technologies."
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/lab_host="E. coli DH108"
/note="Vector: pCMV-SPORT6.0 (invitrogen Technologies);
/site_1: NotI; Site_2: MluI; mRNA obtained from wheat see
of cultivar Glenlea 25 days post-anthesis"
111 c 148 g 168 t
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/clone_lib="TaE25"
/tissue_type="developing seeds"
                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 7.8e+03;
                                                                                                                          Score 22.6; DB 12
Pred. No. 6.2e+03;
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AQ872730
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                                                                                                                                                                 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desktages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Hager, K. analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                               AQ872730 455 bp DNA lin
V15F1 mTn-3xHA/lacZ Insertion Library, strain
cerevisiae genomic 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Rosidae; euroside II; Brassicales; Brassicaceae; Brassica.
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BOMEU91TF BO_2_3_KB Brassica
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BH659639
                              Yale University
P.O. Box 208103, New Haven,
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                  Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell.
                                                                                                                                     Gene Disruption 
Unpublished (1999)
                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; 1 (bases 1 to 455)
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DNA is from a doubled haploid provided
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Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
64 c 110 g 301 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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Class: Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
                                                                                                                                                                                                                                                                                                                                                           Yale University
F.O. Box 208103, New Haven,
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kumar A
Michael Snyder, Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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GSS.
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AQ874006
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                                                                                                                                                                                                                                                                                    primer: GGCCTTCTTTCTTTGGAAGTAC
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                                                                                    /note="Vector: pHSS6-Sal; A yeast genomic DNA library was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lac
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                                                                   minitransposon containing lacz,
                                                                                                                                                        /organism="Saccharomyces cerevisiae"
/strain="AB972 - trp1 r(0) (S288C background)"
/db_xref="feaxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library, strain AB972"
/lab_host="E. coli"
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/strain="AB972 - trp1 r(0) (S288C background)"
/db_xref="reaxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library, strain AB972"
/lab_mst="E. coli"
                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                     108
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Pred. No. 1.1e+04;
0; Mismatches 3;
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                                                                                    o cloning. This a mTn-3xHA/lacZ
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AQ872952/c
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baker's yeast
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325 GCTGTTGTTGCTTCTTGTTC 299
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                                                           AQ872952
V56B3 mTr
AQ872952
AQ872952.1
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P.O. Box 208103, New Haven,
Tel: 203 432 9949
Fax: 203 432 6161
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Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                       cerevisiae genomic
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
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                   578 ]
mTn-3xHA/lacZ Insertion
isiae genomic 5', DNA seq
952
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/strain="AB972 - trpl r(0) (S288C background)"
/db xref="Itaxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library, strain AB972"
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  GI:6285196
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Pred. No. 1.1e+04
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Pred. No. 1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGTTGTTACTTTTCTTCTTCTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTTGTTGCTTTCTTGTTCTGTTC 336
                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                        Grossman, A., Davies, J., Federspiel, N., Harris, B., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants; project phase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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1 (bases 1 to 578)
                                                                                     Durham, NC 27708-1000
                                                                                                                                                Contact: Charles Hauser
                                                                                                                                                                  Vascular Plants; project phase 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                    BG850976.1 GI:14232160
EST.
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1024029H08.yl C. reinhardtii CC-1690, normalized, Lambda
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Location/Qualifiers
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te of mTn-3xHA/lacZ insertion.
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                        chauser@duke.edu
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Location/Qualifiers
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/db_xref="taxon:4932"
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Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
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te of mTn-3xHA/lacZ insertion.
Seq primer: GCCCTTCTTTCGAAGTAC
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203 432 9949
203 432 6161
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/note-"Vector: pHSS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This libra was subsequently mutagenized with a mTn-3xHA/lacZ
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XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
                                                                                              /lab_host="E. coli"
/note="Vector: pHSS
                                                                                                                                               /db_xref="taxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
                                                                                                                                                                                          organism="Saccharomyces cerevisiae"
/strain="Y2278 - S288C background, c
                                                                                                                                                                                                                                                                       Location/Qualifiers
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ALIGNMENTS

chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus 05-OCT-2000. Synthetic transgenic plant; ss Guide desoxynucleotide building block G3 19-FEB-2001 AAA96851; AAA96851 standard; DNA; 31 BP 29-MAR-1999; 29-MAR-2000; 2000WO-IB00370 WO200058485-A1 Promoter; intergenic region; Commelina yellow mottle virus; MERISTEM THERAPEUTICS (first entry) 99FR-0003925

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Human cDNA sequenc Bacillus lichenifo Human foetal liver

Chimeric expression promoter for transgenic plant production, comprises

WPI; 2000-647238/62.

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Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and first second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.
                      The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue
                                                                                                                                                                                                                                                                                                          Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate
                                                                                                                                                                                                                           Example 4;
                                                                                                                                                                                                                                                                             of most human
                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ61194 standard; DNA; 339 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a guide desoxynucleotide building block, which was used to link directional desoxynucleotide building blocks during construction of chimeric promoters of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription product; genetic markers; tagging; in vivo; scription; mapping; locations; chromosomes; chromosomal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCCACCTTTTACATTCCCGCCTTTCATTG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
     of disease-associated for prepn. of antisens
                                                                                                                                                                                                                        Page 452; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Moreno RF,
                                                                                                                                                                                                                                                                                                    human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 5 A; 11 C; 2 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                             genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9208-0837195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US01294
of antisense sequences,
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Pred. No. 0.0007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST01232
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Claim 3; Page 359; 546pp;

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                                                                                          Feng P,
Kayw H,
                                                                                                                                                                                               24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
                                                                                                                                                                                                                                                 24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; renal disease; lymphoma; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; prostate disease; obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease; lung disease; thymus disease; digestive disorder; endocrine disorder; lung disease; thymus disease; digestive disorder; endocrine disorder;
                                                                                                               Brewer
                             New isolated human genes and the secreted
                                                  WPI; 1999-303069/25
P-PSDB; AAY19534.
                                                                                                                                                                                                                            24-OCT-1997;
24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              infection; AIDS; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1999
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                                                                                                                                   (HUMA-)
                                                                                                                                                                             24-OCT-1997
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                                                                                            f LA, the Florence of
                                                                                                                                   HUMAN
                                                                              Lafleur DW, Moore PA,
I, Shi Y, Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                  GENOME
                                                                                                                                                                                              97US-0063098.
97US-0063099.
97US-0063100.
97US-0063101.
97US-0063109.
                                                                                                                                                                                                                                                 97US-0063090.
97US-0063091.
97US-0063092.
97US-0063097.
                                                                                                                                                                           97US-0063110.
97US-0063111.
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                                                                                                                                  SCI INC
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                                                                                                    Ebner R,
Greene J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                 i J, Olsen
Y, Young
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                                                                                                     ű,
                              polypeptides they encode
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                                                                                 P;
                                                                                                              Endress GA;
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RESULT 4
ABL29926/c
ID ABL299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malignancies, diseases of testes, lung or thymus, digestive disorders, infections and AIDS. The polypeptides are also identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila
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   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG18176-ABL30511), expressed DNA sequences (ABLG18176-ABL30511).
                                                                                                                                                                                                                                                      Claim 1;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                         detection, reagent for for elucidating cell s
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signalling
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    RESULT 5
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                         The present sequence is the genome sequence of Listeria monocytogenes BGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072).
The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                  Genomic sequence for Lister and prevention of Listeria related polypeptides
                                                                                                                                                                                                                                                                                                                                                                             Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40962 BP; 12314 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA03041 standard; DNA; 2944528
                 organisms
                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1; 192pp; French.
                                                                                                                                                                                                                                                                                                                                    WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                  Rose
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The sequence data
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   for this
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Cossart P;
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ABL66989/c
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27-SEP-2000
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28-SEP-2000
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                         Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2944528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                     30-MAY-2001;
                                                                                                                                                                                                                                                                                                                     13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                        Thyroid cancer related gene sequence SEQ ID
                                                                                                                                                                                                                      22-SEP-2000;
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Similarity 80.0%;
24; Conservative
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                                                                2000US-236842P.
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2000US-234567P.
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0; Mismatches
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29-JUL-1999; 27-AUG-1999; 11-JAN-2000; 02-MAY-2000;

99JP-0248036. 99JP-0300253. 2000JP-0118776. 2000JP-0183767.

28-JUL-2000;

2000EP-0116126

EP1074617-A2

Homo sapiens

07-FEB-2001.

Human; primer;

detection; diagnosis;

antisense therapy; gene therapy;

88

Human cDNA sequence SEQ ID NO:11429

AAH14182;

26-JUN-2001

(first entry)

AAH14182 standard; cDNA; 3079

ВP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical cagent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 (CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC casophageal, ovarian, kidney, prostate or pancreatic cancer, cc infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
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Best Local S
Matches 24
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03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237608P.
03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
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Soppet DR,
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l Similarity 77.4%;
24; Conservative
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Weaver Z
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Pred. No. 60;
0; Mismatches
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RESULT 8
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                      1217
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Ishii
                          05-OCT-2001; 2001WO-US31437
                                                                                                                              Bacillus licheniformis
                                                                                                                                                                                          Differential gene expression; genomic sequenced tag; GST
                                                                                                                                                                                                                    Bacillus licheniformis genomic sequence tag
                                                                                                                                                                                                                                                         13-AUG-2002
                                                                                                                                                                                                                                                                                                                     ABK76620 standard; DNA; 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 5602 nucleotide sequences defined in the specification, oligonucleotide comprises at least 15 nucleotides; or (b) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
06-OCT-2000; 2000US-0680598
                                                               11-APR-2002
                                                                                                                                                          physiological provocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 11429; 2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000; 2000JP-0241899
                                                                                                                                                                           altered culture
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                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCCACCTTTTACATTCCCGCCTTTCATTG 31
                                                                                                                                                                                                                                                                                                                                                                                                    ATACCATTTTTTAAAGTCCCACCTTTCAATG 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               890 A; 664 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu
                                                                                                                                                            de.
                                                                                                                                                                           environmental
                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.8;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 G; 950 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K,
A, Nagai l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>7
                                                                                                                                                                                                                         (GST) #3911.
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Ctsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 9
ABA61610/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of
04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the method of the invention.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                    Human foetal liver single
                                                                                                                                                                                                                                                        01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monitoring differential expression of several genes in first Ba cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                               30-JAN-2001; 2001WO-US00669
                                                                                                                   WO200157277-A2
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                   Human; foetal liver;
                                                                                                                                                                                                                                                                                         ABA61610;
                                                                                                                                                                                                                                                                                                                         ABA61610 standard; DNA; 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information available. This sequence represents a genomic sequence tag (GST) used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 3911; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequenced tag array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-416684/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berka R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO) NOVOZYMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 96 A; 55 C; 39 G; 101 T; 0 other;
                                                                                                                                                                                                                                                    (first entry
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AS.
                                                                                                                                                                                   gene expression; single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.6%;
79.3%;
                                                                                                                                                                                                                    exon nucleic acid probe #9915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.4;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Length 291;
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                                                                                                                                                                                   acid
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                                                                                                                                                                                   probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 10
ANI41521/c
ID ANI415
XX ANI415
XX Probe
XX W02001
XX W02001
XX W02001
XX W01-FEI
PR 03-AUC
XX W01-FEI
PR 04-FEI
PR 03-AUC
XX W01-FEI
PR 04-OCT
XX W01-FEI
PR 04-O
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Best Local S
Matches 23
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21-SEP-2000;
27-SEP-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                WPI; 2001-488897/53
                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from humar fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI41521 standard; DNA; 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
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                                                                                                                           (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                           MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595
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                                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
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                                                                                                                                                               ; 2000US-0180312.
2000US-0207456.
2000US-0608498.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-023659.
; 2000US-023659.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 9915; 639pp + sequence listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                   尺,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; placenta; antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.6%;
                                                                                   Chen
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                                                                                   Σ
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Pred. No. 91;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 G;
                                                                                 Rank
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a sample derived from h
                                                                                   뮸
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595;
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RESULT 11
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Best L
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207777P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
27-DEC-2000; 2000US-253629P.
16-FEB-2001; 2001US-269308P.
       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa aureus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying get expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                 Haselbeck R, Yamamoto RT,
                                                                                                                                           New polynucleotides antibiotics, compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ds; prokaryotic antibiotic; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                     Claim 27;
                                                                                                                                                                              P-PSDB;
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79.3%;
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21-APR-1995;
07-JUN-1995;
readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFS) of the Haemophilus genome. The EMFS can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       programmes. The antisense nucleic acid sequence is also useful to scree for homologous nucleic acids which are required for cell proliferation a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
medium - useful for ic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-)
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                                                                                                                                                                                                                                 This sequence
                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                           This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams MD,
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79.3%;
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                                                                                           The invention relates to a genetically-engineered outer membrane vesicle (bleb) preparation from a Gram-negative bacterium for use as a vaccine. The blebs of the invention are improved with respect to their imunogenicity and toxicity by the introduction of one or more genetic imunogenicity and toxicity by the introduction of one or more genetic changes to the changes made include the upregulation of protective antigen expression, the downregulation of immunodominant non-protective antigen expression, and genetic changes which result in detoxification of the chipid A moiety of lipopolysaccharide (LPS). The invention also encompasses modified Gram-negative bacterial strains from which the bleb preparations are made, a vector suitable for performing recombination events (for the generation of the modified bacterial strains) and an immunoprotective and non-toxic Gram-negative bleb ghost, or killed whole call vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a medicament for immunising a human host against a considerations, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella.
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          meningitidis, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella catarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia pneumonia. The invention may also be used to provide immunisation against the influenza virus. Bacterially derived nucleotide sequences of the invention are used in the performance of homologous recombination events up to 1000 by upstream of a bacterial chromosomal gene in order to either
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 83; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination
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Thiry G,
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expression of that
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Pred. No. 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dequesne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lobet Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
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RESULT 14
ABK37780/c
             derived from a pathogen capable of protecting a host against the pathogen, mixed with an adjuvant comprising a bleb preparation derived from a Gram-negative bacterial strain. The immunogenic composition consists of N. meningitidis B blebs or N. meningitidis C polysaccharide antigen. The blebs (derived from the outer membrane) may also have their toxic lipopolysaccharide (LPS) content reduced using heterologous down regulating sequences for LPS pathway genes or by up regulating genes involved in LPS synthesis suppression, by the pregulating genes involved in LPS synthesis suppression, by a promoter replacement technique. The immunogenic preparation is useful in the manufacture of a medicament for the treatment of a disease caused by the pathogen from which the antigen is derived (e.g. from Valeseria, meningitis and bacteraemia, from Moraxella, otitis media and pneumonia, and from H. influenzae chronic bronchitis, sinusitis, preparation composition comprising one or more pneumococcal capsular polysaccharides or protein antigens. The present sequence is a strong constrained to the present sequence is a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic composition comprising an antigen derived from a pathogen and a bleb preparation from Neisseria meningitidis, useful a vaccine for treating or preventing disease caused by the pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an immunogenic composition comprising an antiger derived from a pathogen capable of protecting a host against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001; 2001WO-EP08857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoet; ds; Antibacterial; vaccine; bleb; Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide; meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis; sinusitis.
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2001GB-0003170.
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constituitively expressing
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Pred. No. 1.
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a Neisseria
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RESULT 15
AAF91399/c
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CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.

CC The blebs of the invention are improved with respect to their immunogenicity and toxicity by the introduction of one or more genetic changes to the chromosome of the bacterium from which the blebs are compared to the changes made include the upregulation of protective antigen expression, the downregulation of immunodominant non-protective antigen compared moiety of lipopolysaccharide (LPS). The invention also capression are made, a vector suitable for performing recombination compared are made, a vector suitable for performing recombination compared the generation of the modified bacterial strains from which the bleb greparations are made, a vector suitable for performing recombination compared to the generation of the modified bacterial strains).

CC events (for the generation of the modified bacterial strains) and an immunoprotective and non-toxic Gram-negative bleb ghost, or killed whole cell vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a medicament for immunising a human host against a client of the compared by infection of one or more of the following: Neisseria gnorrhoeae, Haemophilus influenza, Moraxella componia. The invention may also be used to provide immunisation against the influenza virus. Bacterially derived nucleotide sequences of the cinemanisation against the influenza virus. Bacterially derived mucleotide sequences of the componia to the performance of homologous recombination events.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified Gram-negative bacterium; outer membrane vesicle; bleb; genetically modified; protective antigen expression; LPS detoxi: LPS; lipid A; homologous recombination vector; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berthet FJ,
Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 46; Page 83; 128pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-138654/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                     microbial infections
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                                                                                                                                                                                                                                                                                                                                                                 invention relates to a genetically-engineered
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87.5%;
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Pred. No. 1
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et P;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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    Score
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18
19
19
19
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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31
1 attccaccttttacattcccgcctttcattg
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Gapop 10.0 , Gapext 1.0
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    Copyright
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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             GenCore version 5.1.5 (c) 1993 - 2003 Compugen
          SUMMARIES
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Sequence 308, App
Sequence 26, Appl
Sequence 26, Appl
Sequence 195, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 147, App
Sequence 147, App
Sequence 117, App
Sequence 101, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 24, Appl
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US-08-998-416-308
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ALIGNMENTS	US-09-227-357-44	US-09-276-531-92	US-09-146-053-6	US-08-899-595-5	US-08-899-595-4	US-09-323-735-1	US-09-080-897-1	US-09-669-974-1	US-09-377-155-1	US-09-232-149A-21	US-09-352-616A-21	US-09-439-313-21	US-09-605-785-21	US-09-030-607-21	US-09-020-956-21	US-08-909-965C-16	US-09-453-702B-60	US-07-792-885A-2
	Sequence 44, Appl	Sequence 92, Appl	Sequence 6, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 21, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 21, Appl	•	•	Sequence 16, Appl	Sequence 60, Appl	Sequence 2, Appli

WIND THE PROPERTY

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DBC-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DBC-1996
ATTORNEY/AGENT IMFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPAX: 919-541-8689 Sequence 308, Patent No. 62 TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 856 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebisching, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG CORRESPONDENCE ADDRESS: ADDRESS: No. 6239264artis Corporation NUMBER OF SEQUENCES: STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina 27709 Application US/08998416 USA Pohlmann, Rainer Steiner, Sabine Philippsen, Peter PAG1251UP DNA (genomic) 1152

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US-09-064-693A-26/c
; Sequence 26, Application US/09064693A
; Patent NO. 6210937
; GENERAL INFORMATION:
; APPLICANT: Ward, Thomas E.
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                                                                                      RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ward, Inc.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: Ward, Thomas E. TITLE OF INVENTION: DEVELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 7.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                  LENGTH: 1348 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: W. Gary Goodson
REGISTRATION NUMBER: 22
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 1625
CITY: Idaho Falls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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5. 6210937
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                                                                                                                                                                                             l Similarity
21; Conserv
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INEEL--Lockheed Martin Idaho
Technologies Co.
                                                                                                                                                                                                                                                                                                                                                                       (208) 526-9469
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                                                                                                                                                                                                         61.9%;
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DEVELOPMENT OF GENETICALLY
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Pred. No. 20;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 195, Application US/08961527
Patent No. 6420135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (208)526-8339
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Toshiba Satellite Pro T2150CDS
COMPUTER: Windows95
                                                                 COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2712 CTTTTACAGTGCCGCCTTTGATTG 2689
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: W. Gary Goodson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 7.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Technologies Co. STREET: P.O. Box 1625
CITY: Idaho Falls
                              APPLICATION NUMBER: US/08/961,527 FILING DATE:
                                                                                                                                                                                                        STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 61.9%;
Local Similarity 87.5%;
                  CLASSIFICATION:
                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CTTTTACATTCCCGCCTTTCATTG 31
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                                                                                                                                                                                                                                                             Human Genome Sciences, Inc
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INEEL--Lockheed Martin Idaho
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                                                                                                                                        Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGINEERED BACTERIA FOR PRODUCTION OF A SPECIFIC PLASTICS PRECURSOR
                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/064,693A
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                                                                                                                           3.50 inch, 1.4Mb
5/33
                                                                                                     version 6.2
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Pred. No. 2
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                                                                                                                                        storage
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER:

FILING DATE:

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Matches 23; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                   TELEFAX: (415) 327-3231 (INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 00 FILING DATE: 29-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: U$/08/619,812
PILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMB: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492
                                                                              LENGTH: 2465 base | TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER OF SEQUENCES:
                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,208
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                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
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NAME/KEY: CDS
LOCATION: 108..1850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALO ALTO
                                                                                                                                                                                                                                                      ROBINS, ROBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6693 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 BRYANT STREET
                                                                                                                   2465 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                 DNA (genomic)
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76.7%;
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Pred. No. 3
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                                                                                                                                                                                            US-08-619-554-3
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                                                                 Matches
                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: COPPOLA. JOSEPH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 07065
                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COPPOLA, JOSEPH REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
   1 ATTCCACCTTTACATTCCCGCCTTTCATTG 31
                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 3, Application US/08619554
No. 5821353
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: SYNTHASE SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION:
                                                                                                                                                                                                                                                                                                                                                   7070 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: JOSEPH A. COPPOLA - MERCK & CO., INC. 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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MORIN, Nancy, - REGISTER, E.A
ONISHI, Janet, - SHEI, Gan-Ju
VENTION: DNA ENCODING 1,3 BETA-D GLUCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732-594-4720
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CLEMAS, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELLY, Rosemarie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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78.6%;
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                                                                                            Score 18.2;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.4;
Pred. No. 40
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                                                                 Mismatches
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                                                                                                                             DB 1;
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                                                                                                                          Length 7070;
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                                                                                                                                                                                                                                                                     RESULT 8
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                                                                                                                                                                                                                                        Sequence 145, Application US/09071035
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent No. 6448043
ENERAL INFORMATION:
                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                249 ATTTCACCTTTTAATTTACCGTCTTT 224
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                                                                                                                                                                                                                                                                                                                                                                  Local 5.
                                                                                                                                                                                              PPLICANT: Gil H. Choi
                                                                                                                                                                 THE OF INVENTION:
COMPUTER: HP Vectra
OPERATING SYSTEM: MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: A. Anders Brookes REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                              MEDIUM TYPE:
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                                                                      OUNTRY:
                                                                                                                                 DDRESSEE:
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                                                                                                                                                                                                           INFORMATION:
                                                                                                     Rockville
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                                                                                         Maryland
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                                                                         USA
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                                                                                                                                  Human Genome Sciences, Inc.
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                             Diskette, 3.50 inch, 1.4Mb storage
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NO: 147:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double
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80.8%;
MSDOS version 6.2
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Pred. No.
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48;
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Query Match
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                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 941.
STREET: 941.
CITY: Rockville
CTATE: Maryland
TGA
                                                                                                 SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: PH
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                         STRANDEDNESS:
                                                                                                                                              TELEPHONE:
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                                                                       502 base pairs
ucleic acid
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80.8%;
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58.1%;
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Score 18;
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DB 3;
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Length 502;
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RESULT 11
US-09-328-111-101/c
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                                                                                                                           Patent No. 6204...
Patent No. 6204...
Patent INFORMATION:
                                                                                                                                                                      Sequence 101,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
             APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J. APPLICANT: Derti, Adnan
                                                                                         APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                        10612 CCACCTTTGAGATGTCCGCCTTTGAT 10587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders REGISTATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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ADDRESSEE: Human Gen
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TOPOLOGY: 11
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DEDNESS: double
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9410 Key West Avenue
                                                                                                                                                                         Application US/09328111
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Pred. No. 1.1e+02;
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; ORGANISM: Paenibacillus amylolyticus
US-09-397-885-2
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 2
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Patent No. 6323007
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(685)
OTHER INFORMATION: n = A,T,C or G
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                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1999-09-17
EARLIER APPLICATION NUMBER: PA 1998 01173
EARLIER FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: PA 1998 01623
EARLIER APPLICATION NUMBER: 60/101,615
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-09-24
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APPLICANT: Monahan, John B.
APPLICANT: Schiegel, Robert
TITLE Schiegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILLING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 5540.200-US
CURRENT APPLICATION NUMBER: US/09/397,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moller, Soren
APPLICANT: Johansen, Charlotte
APPLICANT: Schafer, Thomas
APPLICANT: Ostergaard, Peter Rahbek
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EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/111,675 EARLIER FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: A 2,6,-b-D-Fructan Hydrolase Enzyme And
TITLE OF INVENTION: Process For Using The Enzyme
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                ENGTH:
2584 CAACATTCACATTCCCGCCTTTTA 2561
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                                       5 CACCITITACATICCCGCCTITCA 28
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Pred. No. 67;
0; Mismatches
                                                                                               Score 17.6;
Pred. No. 1
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                                                                             Mismatches
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RESULT 13 US-09-058-489-29

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Whitehead Institute for Biomedical Research APPLICANT: Lahn, Bruce APPLICANT: Page, David TITLE OF INVENTION: Genes in the No. 6103886-Recombining TITLE OF INVENTION: the Y Chromosome FILE REFERENCE: WHI97-08pA
                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1202
                SEQUENCE CHARACTERISTICS:
LENGTH: 5300 base pairs
TYPE: nucleic acid
                                                                                                                                    REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/75
APPLICATION NUMBER: 08/75
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nguyen, Thai D. APPLICANT: Polansky, Jon R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 ACTCAACATTTACATTCCATCTTTC 674
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                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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5. 6171788
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                                                                                                                     202 383-6610
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77.8%;
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Pred. No. 1.1e+02;
0; Mismatches 6;
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                                                          Query Match
-- rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application Patent No. 6171788
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Best Local Similarity
                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5304 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791
PILING DATE: 28-JAN-1997
ATTORNEY AGENT INFORWATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
 2573
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2573 TrGCCCTTTCACCTTCCTGCCTTCA 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nguyen, T
APPLICANT: Polansky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                       TELEFAX: 202 383-6610
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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TTGCCCTTTTCACCTTCCTGCCTTTCA
                           TTCCACCTTTTACATTCCCGCCTTTCA 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Howrey & Simon
1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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77.8%;
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77.8%;
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                                                                        Score 17.4;
Pred. No. 1
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Pred. No. 1.
                                                    Pred. No. 1.400; Mismatches
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                                                                                    Length 5304;
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Search completed: May 11, Job time : 16.4311 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       seq length: 0
seq length: 2000000000
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1: /cgn2 6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2-6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2-6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2-6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2-6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2-6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

6: /cgn2-6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2-6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2-6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

9: /cgn2-6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2-6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

11: /cgn2-6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

12: /cgn2-6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2-6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

14: /cgn2-6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
         May 11, 2003, 03:08:16; Search time 30.6892 Seconds (without alignments) 1255:289 Million cell updates/sec
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31
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9 US-10-067-514-1

10 US-09-960-352-14643

10 US-09-964-824A-23

11 US-09-964-761-15272

10 US-09-915-242-6926

9 US-09-918-842A-4351

10 US-09-918-842A-4351

10 US-09-918-8653

9 US-09-796-692-8653

9 US-09-796-692-8653

10 US-09-822-849A-431

10 US-09-822-849A-431

10 US-09-764-891-9791

10 US-09-764-891-9791
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Sequence 17, Appl Sequence 1, Appli Sequence 23, Appl Sequence 15272, A Sequence 15272, A Sequence 626, App Sequence 626, App Sequence 6431, App Sequence 8653, App Sequence 8653, App Sequence 8791, App Sequence 3791, App S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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RESULT 2
US-10-67-514-1/c
US-10-67-514-1/c
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Jonsdottir, Sif

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1 ATTCCACCTTTTACATTCCCGCCTTTCATTG 31

Query Match Best Local S Matches 31

Similarity

100.0%;

Score 31; Pred. No. Mismatches

0.0014; В

0;

Indels

0

Gaps

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9; Length 31;

31;

Conservative

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RESULT 1 US-09-963-803-17 ; Sequence 17, Application US/09963803 ; Publication No. US20030028922A1 ; GENERAL INFORMATION: APPLICANT: Meristem Therapuetics ITILE OF INVENTION: Chimeric expression promoters of TITLE OF INVENTION: Virus and cassava vein mosaic CURRENT APPLICATION NUMBER: US/09/963,803 ; CURRENT FILING DATE: 2001-09-26 ; PRIOR APPLICATION NUMBER: FR 99/03925 ; PRIOR FILING DATE: 1999-03-29 pRIOR FILING DATE: 1999-03-29 ; PRIOR FILING DATE: 2000-10-05 ; NUMBER OF SEQ ID NOS: 39 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 17 LENGTH: 31 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Guide desoxynucleotide buildin; OTHER INFORMATION: block G3 US-09-963-803-17	20 18.4 59.4 1039 7 US-08-781-986A-273 c 21 18.2 58.7 10 US-09-974-300-249 c 22 18.2 58.7 108 10 US-09-974-300-7471 c 23 18.2 58.7 293 10 US-09-938-718A-5 c 25 18.2 58.7 5230 10 US-09-838-718A-6 c 26 18.2 58.7 5970 10 US-09-838-718A-6 c 27 18.2 58.7 5900 10 US-09-838-718A-6 c 27 18.2 58.7 9412 9 US-10-032-393-52 18.2 58.7 9412 9 US-10-032-393-48 31 18.2 58.7 9417 9 US-10-032-393-17 29 18.2 58.7 9417 9 US-10-032-393-48 31 18.2 58.7 9437 9 US-10-032-393-49 33 18.2 58.7 9437 9 US-10-032-393-49 34 18.2 58.7 9566 9 US-10-032-393-7 35 18.2 58.7 10929 9 US-10-032-393-7 36 18.2 58.7 10929 9 US-10-032-393-7 c 39 18.2 58.7 12733 9 US-10-032-393-49 c 39 18 58.1 274 10 US-09-078-574-13572 c 40 18 58.1 274 10 US-09-078-574-8758 c 41 18 58.1 724 10 US-09-079-77A-832 c 41 18 58.1 724 10 US-09-079-57A-832 c 44 17.8 57.4 362 9 US-10-040-862-6999 c 44 17.8 57.4 362 9 US-10-040-862-6999
moters originating from commelina yellow	Sequence 273, App 249 Sequence 249, App 7471 Sequence 249, App 1-5 Sequence 209, Ap 1-7 Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 52, Appl Sequence 52, Appl Sequence 48, Appl Sequence 48, Appl Sequence 49, Appl Sequence 17, Appl Sequence 50, Appl Sequence 51, Appl Sequence 50, Appl Sequence 17, Appl Sequence 17, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 13572, Appl Sequence 1377, App Sequence 137, App Sequence 137, App Sequence 931, App Sequence 931, App Sequence 931, App Sequence 6999, Ap

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                                                                                                                                                                                                       Sequence 23, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturities OF INVENTION: Sets
FILE REFERENCE: 689290-73
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local
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                 CURRENT APPLICATION NUMBER: US/09/964,824A CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR ETILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR FILING DATE: 2000-09-28
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLESIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Clone ID: 62-LIB34-082-Q1-E1-H10
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SEQ ID NOS:
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85.2%;
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Pred. No. 1.1e+02;
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Matches
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LENGTH: 291
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL I
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                              Patent No.
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TITLE OF INVENTION: Methods For Monitoring Multiple
TITLE OF INVENTION: Expression
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APPLICANT: Clausen, Ib G:
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LOCATION: (1)...(498)
OTHER INFORMATION: n=a,t,g
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                                                                                                                                                                                                                                                                                                            INFORMATION:
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Pred. No. 92;
0; Mismatches
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Pred. No. 69;
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FOR

APPLICATION NUMBER: PCT/US01/00666

2000-10-04 NUMBER: US 2000-09-27

US 60/236,359

APPLICATION NUMBER: FILING DATE: 2000-0

APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04

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         TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITEA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
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LENGTH: 595
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION: MAP TO AC018469.3
OTHER INFORMATION: EXPRESSED IN FETAL
OTHER INFORMATION: EXPRESSED IN PLACE
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: US 09/774,203
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FILING DATE:
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Trawick, John D.
                                                                                                                                                                 Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Pred. No. 1e+02;
); Mismatches
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                                                                                                                                                 Essential Genes
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RESULT 9 US-09-783-590-526/c

Sequence 526, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.

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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1671)
US-09-815-242-6926
                                                                                                                                   US-09-938-842A-4351
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                                                                               Query Match
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                                                                                                                                             TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                  ENGTH:
1704
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TTCCCATTTTGCATTCCCTCCTTTCGTT 1676
                              TTCCACCTTTACATTCCCGCCTTTCATT 30
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5. US20020160378A1
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                                                               Conservative
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79.3%;
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                                                                                                 Score 19.4;
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Pred. No. 1.2e+02;
                                                                                   Pred.
                                                               Mismatches
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NUMBER
SOFTWARE: Pater
SEQ ID NO 526
FNGTH: 501
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CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT TILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILLING DATE: 1995-04-12
PRIOR FILLING DATE: 1994-11-21
PRIOR FILLING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                             LOCATION: (402)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (74)
OTHER INFORMATION: n equals
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                   LOCATION: (375)
OTHER INFORMATION: n equals
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LOCATION: (345)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY? misc feature
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PPLICANT: Ruben, Steven M.
ITLE OF INVENTION: Human Genes, Sequences,
ILE REFERENCE: PO-16.2C1
                                                   OTHER INFORMATION: n equals
                                                                                                                                                                                               OCATION: (374)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
                                   NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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JOCATION: (351)
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                                                                      OCATION:
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INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                Sequence 8653, Application US/09796692 Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                           APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TILE REFERENCE: 2017.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
                                                                                                                                                                                                                  GENERAL INFORMATION:
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               APPLICATION NUMBER: 60/190,479 FILING DATE: 2000-03-17
APPLICATION
                                                FILING DATE:
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Pred. No. 1.4e
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APPLICATION NUMBER: 60/200,779

2000-04-27

60/200,303

APPLICATION NUMBER:

60/200,999

FILTING DATE

NUMBER:

60/206,201

2000-05-22 2000-05-04 2000-05-01 2000-04-28 2000-04-28

NUMBER: 60/202,084

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                                                                                                        US-09-796-692-8653
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LENGTH: 493
                                                                        Query Match
                                               Matches
                                                                                                                                 NAME/KEY: unsure
LOCATION: (486)
                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (389)
OTHER INFORMATION: n=A,T,C or
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LOCATION: (158)
OTHER INFORMATION: n=A,T,C or
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                                                                                                                   THER INFORMATION: n=A, T, C or G
                                                                                                                                                                             VAME/KEY: unsure
LOCATION: (465)
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OTHER INFORMATION:
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.OCATION: (225)
YTHER INFORMATION: n=A,T,C or
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OTHER INFORMATION:
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ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                OCATION: (386)
OTHER INFORMATION: n=A,T,C or
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JOCATION: (332)
WHER INFORMATION: n=A,T,C or
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OCATION: (279)
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OCATION: (252)
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                                                           Local Similarity
1 ATTCCACCTTTTACATTCCCGCCTTTCATTG 31
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                                               Conservative
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74.2%;
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                                                           Score 18.8;
Pred. No. 1.
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                                            Mismatches
                                                         1.7e+02;
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SEQ ID NO 8653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (117)
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LOCATION: (158)
OTHER INFORMATION:
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LOCATION: (165)
                                                    OTHER INFORMATION:
                                                                                     NAME/KEY: unsure
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LOCATION: (225)
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OTHER INFORMATION:
AME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/796,692
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Retter, Marc
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OTHER INFORMATION: n=A,T,C or

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                                                                                                 ; ORGANISM: Homo sapiens
US-09-822-849A-431
                                                                                                                                                      SOFTWARE: Par
SEQ ID NO 431
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                                                                   Query Match
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
                                                                                                                                                                                                                                   FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                             APPLICANT: AGOSTINO, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wong, Gordon G. APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (486)
OTHER INFORMATION: n=A,T,C or
                                                                                                                              TYPE: DNA
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LOCATION: (308)
OTHER INFORMATION:
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LOCATION: (332)
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THER INFORMATION:
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THER INFORMATION:
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THER INFORMATION:
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CCATION: (465)
THER INFORMATION:
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nes 23; Conser
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         1 ATTCCACCTTTTACATTCCCGCCTTTCATT 30
                                     l Similarity
23; Conserv
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ilarity 74.2%;
Conservative
                                     Conservative
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                                    Score 18.8; DB 10
Pred. No. 1.9e+02;
D; Mismatches 7
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Pred. No. 1.7e+02;
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                                                                DB 10;
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                                                                Length 1038;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3657
; LENGTH: 32192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3657
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US-09-764-891-9791/c
; Sequence 9791, Application US/09764891
; Sequence 9790, US20030077808A1
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US-09-764-891-9791
                                                                                                                                               Sequence 399, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
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"" "ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9791
LENGTH: 32192
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CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-01-17
CURIOT application data reemoved - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed NUMBER OF SEQ ID NOS: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                  NUMBER OF SEQUENCES: 982 CORRESPONDENCE ADDRESS:
                                                                                                              APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                       TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                         23;
ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                       Steven Barash
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76.7%;
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Pred. No. 3.3e
0; Mismatches
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Pred. No. 3.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     3.3e+02;
7;
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COMPUTER READMALE FORM:

REDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER READMALE FORM:

REDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM. MSDOS version 6.2
SOFTMARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/070,927A
ILING DATE: 04-May-2000

LILING DATE: 197-05-06

REPLICATION NUMBER: 05/046,655
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,031
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,032
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,033
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,033
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,033
FILLING DATE: 197-05-16

APPLICATION NUMBER: 06/046,039
FILLING DATE: 197-05-16

APPLICATION NUMBER: 106/046,039
FILING DATE: 106/04/04
FILLING DATE: 106/04/04
FILLING DATE: 106/04/
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 May 11, 2003, 02:48:15; Search time 498.331 Seconds (without alignments) 1007.484 Million cell updates/sec
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31
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Copyright (c) 1993 - 2003 Compugen Ltd.
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em_htc: *
gb_est1: *
gb_est2: *
gb_htc: *
gb_est3: *
gb_est4: *
em_gss_hum:*
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em_gss_pln:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

6	ი 5	C 4	u	2	c 1	Result No.
22	22	22	22	22	22	1
71.0	71.0	71.0	71.0	71.0	71.0	Query Score Match Length
631	614	599	599	570	548	% Query Match Length DB
13	14	13	13	13	13	DB
BM330506	BM952936	BM317907	BM269265	BM334924	BM318384	ID
	: BM952936 952060C11	BM317907 PI1_13_A0	BM269265 MEST407-A	BM334924 MEST130-A	BM318384 PI1_13_A0	Description

ALIGNMENTS

RESULT 1

	COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BM318384/c
The University of Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement.	Contact: Cordonnier-Pratt MM	Unpublished (2000)	,ה.ה. An EST database from Sorghum: pathogen-induced plants	Cordonnier-Pratt, MM., Gingle, A., Dean, R., Sudman, M. and Pratt	1 (bases 1 to 548)	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Sorghum bicolor	sorghum.	EST.	BM318384.1 GI:18052726	BM318384	mRNA sequence.	PI1_13_A02.b9_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,	BM318384 548 bp mRNA linear EST 03-JAN-2002	

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JOURNAL COMMENT
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AUTHORS
TITLE
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BM334924
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KEYWORDS
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rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones Unpublished (2001)
                                                                                                                                                                                                                                                 gmail: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                           Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
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/clone lib="pathogen induced 1 (PII)"
/note="Corgan: Anthracnose-infected leaves from
/note="Corgan: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX-62)
cultīvar) were infected with pathogen (isolate FRM42I of
Collectrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4558"
/clone_lib="Pathogen
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                     Iowa
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Pred. No. 1.6e+02;
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BM269265
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Contact: Patrick S. Schnable Schnable Laboratory Iowa State University
                                                                                                                 Wen, T.J., Qiu, F., Guo, L., Ashlock, D.A and Schnable, P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones Unpublished (2001)
                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the decombase were dispested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pTTTJPAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissues: Germinated seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="mixed"
lab_host="DH10B"
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83.3%;
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Pred. No.
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Zea mays cDNA clone MEST407-A04 3', mRNA
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Agronomy, Iowa State University, Ames,

IA 50011-1010,

USA

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RESULT 4
BM317907/c
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Best Local Similarity
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                                                                                                                 599 bp PII 13_A02.g9_A002 Pathogen indumENA sequence.
                                 BM317907
BM317907.1 GI:18052249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: universal
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phred software,
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Individual basecall and confidence value were assigned using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
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/note="Vector: pT773PAC; Site 1: EcoRI; Site 2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG)
), Tassel (3-39 cm, 53 and 56 DAG), Finature ear (0.2-3.0)
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings,
NAA (a-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, APC
(1-aminocyclopropane-1-carboxylix acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscisic acid)
-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings de-cDNA
molecules were generated as follows. Pirst-strand cDNA
molecules were generated as foll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECORI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

147 c 115 g 178 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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83.3%;
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                                                                                                                                                  y DP mRNA linear EST 03-JAN-2002 induced 1 (PII) Sorghum bicolor cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TTCCACCTTTTACATTCCCGCCTTTCATTG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-72 Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                        mays cDNA,
                                                                                                                                                                                                                                                   952060Cl1.xl.952 - BMS tissue
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Unpublished (2000)
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1 (bases 1 to 599)
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                                                                                        Zea mays
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                                                                                                                           Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of
Colletotrichum graminicola, which is a sorghum isolate)
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the pathogen."
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/db_xref="taxon:4558"
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83.3%;
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ssue from Walbot Lab (reduced rRNA) Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 bp mRI
PIC1 52 H06.gl_A002 Pathogen-infected
bicolor cDNA, mRNA sequence.
BM370F06
Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                        Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                        1 (bases 1 to 631)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                            Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM330506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walbot, V.
Maize ESTs from various
                                                                                                                                                                        Contact: Cordonnier-Pratt MM
                                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                  An EST database from
                                                                                                                                                                                                                                                         Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                          BM330506.1
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Plate: 952060 row: C column:
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706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Organism="Zea mays"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/clone_lib="952 - BMS tissue from Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lab_host="DH10B"
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Pred. No. 1.6e+02;
D; Mismatches 5
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    to exclude PolyA, vector, and regions threshold for highest quality sequence
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compatible 1
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(PIC1) Sorghum
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Email: oandersn@pw.usda.gov
Sequences have been trimmed
quality sequence with phred
Seq primer: SK primer.
                                                                                                                            Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ283489 639 bp mRNA linear EST 13-MAY WHE3091_G03_M05ZS Wheat cold-stressed seedling subtracted cDNA library Triticum aestivum cDNA clone WHE3091_G03_M05, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: T7
                                                                                                                                                                                                                                                                           The structure and function of the expressed genomes - Cold-stressed seedling subtracted
                                                                                                                                                                                                                                                                                                                         Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Crossman,C.,,R.D., Lazo,G.R., Nguyen,H.T., Pham,J., Rausch,C.J., Wilson,J. and Zhang,D.
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                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bread wheat.
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Colletotrichum graminicola"
/note="vector: pBluescript II SK(-) from Lambda Zap II;
Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRM42I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
81 a 120 c 154 g 176 t
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/cultivar="BTX623"
/db_xref="Exacon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
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83.3%;
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Pred. No. 1.6e+02;
0; Mismatches 5
                            to remove vector sequence and low score less than 20
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(<a href="http://depts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                              Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                       Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed Sequence Tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 644)
Qiu, F., Cui, F., Guo, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                              Phred software,
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                         515-294-2299
                                                                                                                                                                                                                                                                                                                                State University
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                                                                                                                                                                                                                                                                                                        Agronomy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing were performed in the OD Anderson lab (all other authors)."
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/db_xref="taxon:4565"
/clone="WHE3091_G03_M05"
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/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Seedling"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:16925592
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                                                                                                                                                                                                                                                                                                      Iowa State University, Ames,
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No. 1.6e+02;
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                                                                                                                                                   Contact: Robert B. University of Utah University of Utah
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25; Conserv
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PCR PRIMERS
PCRWARD: Forward PCR primer sequence, primer T7-1
CTA TAG)
BACKWARD: Backward PCR primer sequence, primer T3
                                                                                                                                                                                                                                                                       ,M., Rose,M., Rose,R., and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            670 bp DNA linear GSS 05-OCT-20110332J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0332J11 F, DNA sequence.
AZ495987
                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0332 row: J column: 1:
                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                  plasmid inserts
                                                                                                                                                                                                                                                     Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ495987.1 GI:10671822
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                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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te: 0332 row: J column: 11 primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genom Research 6: 791-806, 1996)."
                                                                                                                                 Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4577"
/clone="MEST122-F07"
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| ab_host="DH10B"
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                                                                                                                                                                                            Email: schnable@iastate.edu Individual basecall and confidence value were
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including seedlings treated with Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wen,T.J., Qiu,F., Guo,L., Ashiock, J.A. and J. Wen,T.J. Qiu,F., Guo,L., Ashiock, J.A. and J. Stages Expressed Sequence Tags from B73 Maize: various stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

[ (bases 1 to 736)
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{<a true continuous continuo
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                                                                                                                                                                                                                                                                                                                                                            State University
Agronomy, Iowa State University, Ames,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/clone="UUGC1M0332J11"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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mays cDNA clone MEST209-B11 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TTCCACCTTTTACATTCCCGCCTTTCATTG
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Zea mays PCC
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AY108329.1
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
25; Conserv
Maize Mapping
Overgo Probes
                   1 (bases 1 to 920)
1 (bases 1 to 920)
14 (bases 1 to 920)
15 (bolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S. Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                 Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-aminocyclopropane-1-carboxylix acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, ettolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a.Naphthalene accetic acid)-treated seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinetin-treated seedlings, ACPC
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83.3%;
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Pred. No. 1.7e
0; Mismatches
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RESULT 12
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MEDLINE
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                                                                                                                                                                                                                                                                                                                Bioinformatics
Bioinformatics
Control Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J84 bp mRNA wEST00402 Mixed stage, Stratagene (cat. #9 elegans cDNA clone CEMSE75, mRNA sequence. M79865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-APR-2002) Maize Missouri, Columbia, MO 65211, Location/Qualifiers
                                                                                                                                                                                                                                                                    Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                McCombie, W.R., Adams, M.D., Kelley, J.M., FitzGerald, M.G., Utt., T.R., Khan, M., Dubnick, M., Kerlavage, A.R., Venter, J. and Ficaenorhabditis elegans expressed sequence tags identify gene Camilles and potential disease gene homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                               Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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1 24 g 213 t 6 others
                                                                                  /clone lib="Mixed stage, Stratagene (cat. #937006)"
/note="Vector: Uni-ZAP XR; C. elegans mixed stage cDNA
library. Strategene catalog #937006. The library is old
dT primed and directionally cloned in the Uni-ZAP XR
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/db_xref="MaizeDB:637475"
/db_xref="taxon:4577"
/clone="PCO128508"
                                                                                                                                                                 /clone="CEMSE75"
                                                                                                                                                                                organism="Caenorhabditis elegans"
|db_xref="taxon:6239"
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Pred. No. 1.8e+02;
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 21.6;
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Length 384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kumar A
Michael Snyder, Dept. of Mol.
Yale University
P.O. Box 208103, New Haven, C
Tel: 203 432 9949
Fax: 203 432 6161
                                                sequence.
BG355209
BG355209.1
Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                   947040C05.y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Disruption Unpublished (1999)
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AQ500362.1
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                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pHSS6-Sal; A yeast genomic DNA library (lacking mitochondrial DNA) was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance." a 149 c 108 g 188 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \( \text{organism="Saccharomyces cerevisiae"} \) \( \text{db_xref="taxon:4932"} \) \( \text{clone lib="m(\text{n}-3xH)/lacZ Insertion Library"} \) \( \text{lab_host="E. colim} \) \( \text{lab_host="E. colim} \)
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85.7%;
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Pred. No. 2.3e
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Eukaryota;

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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AUTHORS
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                                                                                                                         Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                       Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
clade; Panicoideae; Andropogor
1 (bases 1 to 477)
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AW331076
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Tel: 650 723 2227
Fax: 650 725 8221
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Department of Biological Sciences
Stanford University
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1 (bases 1 to 447)
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ilarity 80.6%;
Conservative
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707047 row: A column:
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grown."
a 78 c 112 g 120 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
Site_1: EcoRI; Site_2: XhoI; Directionally cloned using
                /organism="Zea mays"
/cultivar="W23"
                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/clone lib="947 - 2 week shoot from Barkan lab"
/tissue type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab host="XL1-Blue"
db_xref="taxon:4577"
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yta; Liliopsida;
                                                                                                                                                           CA 94304, USA
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tissues from Walbot lab (
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BASE COUNT
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163 ATTTCTCCTTTTACTTTCTTGCCTTTCCTTG 133
                      1 ATTCCACCTTTTACATTCCCCGCCTTTCATTG 31
                                                                                                                                                            155
                                                                     Conservative
                                                                                                                                                            Ø
                                                                                                                                                     /note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site 1: EcoR1; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, sil husk, root, leaf). Unidirectionally cloned."

70 c 116 g 136 t
                                                                                                                                                                                                                                                                 /tissue_type="tassel, kernel, silk, husk, root,
/dev_stage="adult"
/lab_host="DH10B"
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80.6%;
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Search completed: May 11, Job time : 502.331 secs 2003, 04:54:34

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS RESULT 1 AX036752 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE Result 0 0 0 0 0 0 0 0000000000000 a a a TITLE ORGANISM ŏ. Score 222 AX036752 Sequence 18 AX036752 artificial sequences. 1 (bases 1 to 32) 1 (constant of the sequences) Rance, I., Theisen, M. and Gruber, V. Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus patent: WO 0058485-A 18 05-OCT-2000; synthetic construct. synthetic construct AX036752.1 Query Match 2898 2898 229061 3103 3103 3134 3438 188616 296320 2996320 2996320 1567 1567 1567 1567 1567 1567 158886 159981 3463 3463 38621 55835 100886 111500 113071 115393 117505 94727 114468 162808 164528 169161 171490 32 116498 Length 188215 from Patent GI:11226261 В AL591034 AC093026 AC021340 AC016800 AR067569 I38521 I56996 I59862 CNS07YPK AC091247 AC096687 AC079778 AL138772 AC019053 AC068209 AR016866 AR020892 CEZK856 AC016944 AF269420 PFU278385 AR064644 AR038502 AR027215 AC006892 ╏ WO0058485 ALIGNMENTS å DNA linear Z70783 Caenorhabdi AC016494 Homo sapi AL161899 Human DNA AC025725 Caenorhab AC025725 Caenorhab AC084158 Caenorhab AC084158 Caenorhab AC084158 Caenorhab AC084158 Sequence AR020892 Sequence AR020892 Sequence AR027215 Sequence AR067569 Sequence 138521 Sequence 10 159862 Sequence 10 159862 Sequence 10 175189 Sequence 10 175189 Sequence 10 AL591034 Human DNA AC093026 Homo sapi AC01903 Homo sapi AC019050 Homo sapi AC019050 Homo sapi AC019078 Homo sapi AC019078 Homo sapi AC01786 Sequence AJ278385 Penicilli AC007786 Homo sapi AC016800 Homo sapi AC016801 Sequence AJ278385 Penicilli AC017785 Sequence AJ278385 Penicilli AC017786 Homo sapi AC017785 Sequence AJ2783778 Homo sapi AF269407 Staphyloc AX145215 Sequence AF270201 Staphyloc AX145275 Sequence AF2703331 Cryza sat AC091247 Cryza sat AC091247 Cryza sat AC091247 Cryza sat AC091247 Cryza sat AX036752 Sequence AL606449 Oryza sat AC123085 Rattus no AL645908 Mouse DNA AL645943 Mouse DNA commelina yellow Description PAT Homo 16-NOV-2000 sapi

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                                                                        NOTE: This is a PHASE2 sequence. Gaps are shown by mnnnn. Genes were identified by a combination of several methods: Gene prediction programs including Figeness (http://www.softberry.com/), genscan (http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GENSCAN.html), GeneMarkHMM (http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.

* NOTE: This is a 'working draft' sequence. It currently 'consists of 2 contigs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the spass between them are based on estimates that have 'This sequence will be replaced to replaced to replaced with sequence will be replaced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USUNUUUU4 116498 bp DNA linear Oryza sativa chromosome 4 clone OSJNBa0014F04, *** PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JUN-2002) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: phrap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone: OSJNBa0014F04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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by the finished sequence as soon as it is available and the accession number will be preserved.

1 62574: contig of 62574 bp in length
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|db_xref="taxon:32630"
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VERSION
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Falls, T. Ferragutc, D., Flagg, N., Ford, J., Fastler, P., Frantz, P., Falls, T. Ferragutc, D., Flagg, N., Garra, N., Gill, R., Gorrell, J.H., Gaveara, W., Gunaratne, P., Hale, S., Hamilton, K., Gorrell, J.H., Gaveara, W., Gunaratne, P., Hale, S., Hamilton, K., Grorrell, J.H., Garra, N., Gill, R., Gorrell, J.H., Gaveara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Hartis, K., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Harris, C., Harris, K., Havlak, P., Hawes, A., Hernandez, J., Homei, T., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Licharge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Li, J., Li, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Wahsens, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Maner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Moyren, N., Nguyen, N., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwetson, N., Nguyen, A., Nguyen, N., Steoner, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tand, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ushani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, F Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delyado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Colling, C., Colling, C., Colling, C., Colling, M., Colling, C., Collin
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1.
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62775 11649
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5 116498: contig of 53724
Location/Qualifiers
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'sub_species="japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Oryza sativa"
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Pred. No. 1.5e+02;
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Center: Baylor College of Medicine, One Center Center Center
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 114513 bases at least Q40
Consensus quality: 117131 bases at least Q30
Consensus quality: 119267 bases at least Q20
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Center clone name: CH230-909
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries thunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 7, 2002 this sequence version replaced gi:17976640. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
1 CAAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-24A24 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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108006
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/clone_lib="RPCI-23"
43879 c 41691 g 58484 t
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                                                                                                                                                                                                                                                                            organism="Mus musculus"
/db_xref="taxon:10090"
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81.2%;
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contig of 3621 bp in length
gap of unknown length
contig of 3352 bp in length
gap of unknown length
contig of 4795 bp in length
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Pred. No. 1.4e.
0; Mismatches
                                                                       0
                                                                                          Score 22.4; DB 10;
Pred. No. 1.4e+02;
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                                                                    Mismatches
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DEFINITION CEZK856

CEZK856 41502 bp DNA linear IN Caenorhabditis elegans cosmid ZK856, complete sequence.

INV 24-JAN-2002

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89603 CAAGTGTTTGAAATAAAGGAGTAAACTAGGGA 89572
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Best Local :
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                                                                                                                     2 AAGGGTTCGAAATAAAGGAATAAATTCGTG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                  AAGGGTCCGAAATAAAGGAGCCAATTCATG 70046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-130E22 from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 8, 2002 this sequence version replaced gi:21732076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL645943 213383 bp DNA linear ROD 12-
Mouse DNA sequence from clone RP23-130E22 on chromosome 11,
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1 (bases 1 to 213383)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark,S.
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                                                                                                                                                                                                                                                                                                                                           59658
                                                                                                                                                                                                    Conservative
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/clone_lib="RPCI-23"
48029 c 47605 g 58091 t
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/db_xref="taxon:10090"
/chromosome="11"
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                                                                                                                                                                                                                         68.8%;
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                                                                                                                                                                                                 Score 22; DB 10; Length 213383;
Pred. No. 1.9e+02;
0; Mismatches 5; Indels 0;
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HTG; DNA directed RNA polymerase III; EF-hand; LIN-19; Spingomyelin phosphodiesterase; TAU; Transposase.
Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The end of this sequence (41399. .41502) overlaps with the start sequence Z73969.
For a graphical representation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The true right end of clone ZK856 is at 104 in sequence Z73969.

The start of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone ZK856. It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlapping sections once, or longer becauverlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For a graphical representation of this sequence and its analysis
see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neighbouring submissions.
The true left end of clone ZK856 is at 32458 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         name=ZK856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    start of this sequence (1. .104) overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or longer because we arrange for a small overlap between
                                                                                                      CDNA
                                                                                                                                  fami
                                                                                                                                                                                                                                                                                                 join(2797...2859,2905...3039,3418...3519,3567...3771,3818...3927,3975...4182,4229...4359,4409...4705,4752.4995...5055,5102...5205,5370...5534,5637...6028,6074./gene="ZK856.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Caenorhabditis elegans"
|db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                              note="Similarity with the C.
                                                                                                                                                                                                        'gene="ZK856.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                   clone="ZK856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is NOT necessarily the entire insert of
     ily), Score=118
n EST yk59a3.3
n EST yk59a3.5
n EST yk161g7.5
n EST yk161g7.3
n EST yk462c3.3
                                                                                                                                                                                                                          (2797. .2859,2905. .3039,3418. .3519,3567. .3771, .3927,3975. .4182,4229. .4359,4409. .4705,4752. .5055,5102. .5205,5370. .5534,5637. .6028,6074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing o 41502)
yk59a3.3 comes from this gene yk59a3.5 comes from this gene yk161g7.5 comes from this gene yk161g7.3 comes from this gene yk162c3.3 comes from this gene
                                                                                                                           similarity to Pfam domain: P
Score=1185.1, B-value=0, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or longer because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shorter because we only
                                                                                                                                                                           elegans LIN-19
                                                                                                                                                       PF00888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            we arrange
                                                                                                                                                       9 protein,
(Cullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of.
                                                                                                                                                                                                                            .4952,
.6125)
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.6125)
                                                                                                                                                  gene
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                                                                                                      CDS
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ADKKLEEBQQRAKRYLEMNSPTSGKHMEKÄVIÄLVESFEDTILAECSKLIASKDVERL
GRLYBLIRRTRSGIDTVLKCIDTHIRTEGLNDMRUNARNLSTDERRYVQQLLLMFDKF
SSLYREGFCIDARLITARDKAFRAVVNDSSIFKTEMMNKKGRTLSVESKCABILANYC
CDLLLRKTQLSKKLTSEEIDEKLNQVLLVLKYVENKDVFMRFHRAHLSRRLILEMSADQ
EKEEMMVTKLRECGWESDAVNKLSRHLODIELMKDNSSFKKALTGTNUNKSIADSIN
MKVLNGGAMGRGGSERIRFSLPREBLEDFVERMVFGTANGRFDLECTTFQMAVLFCFN
DRAHDKISLETURLATELPDAELNRTLLSLVAYFKMXQILLCDVPSTTVTAEDFTDS
TKFLLNHDFNVVKNGKSQQRGKVNLIGRLOLSLEANAEKEHSSIVALRELRADD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /proteIn_id="CAA94850.1"
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/db_xref="SPTREMBL:Q23637"
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TSIVHIVAHIGPGVFEKTPNFTWFRDEYNERFLDLTVRYANSIGWMIFGHHHTDTFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGRSKMKSPVKRGRPPNELTKKVLDILYNDEFPVSENQDRFRRQVNVNESAINFNGFN
DIGKMLQGHVTNFNNDIVHFLKKFQKAISVSGRNE"
complement(join(7983. .8215,8261. .8426,8632. .8932,
8984. .9175,9380. .9520,9590. .9715,9760. .9852,9897. .101
                                                                                                                                                                                                                                                    APFGIIRAVQICPIDACQAFVVFQNDYERSARQSVSRLLELTSGTMFVNGYMWTICRP
VKCNHVARTHEEREVEBPGITTSRGVTVDELSGIFASFIQQNSSVSQTSIFSDSTQSF
SSYSLFSRSRTVSSSSSQYAESCDSSATITPPSYYPAQQSTGFLNLPPPYHTLPDTAF
                                                                                                                                                                                                                                                                                                                                                                             IKDSKENNVQLALMAPAVTPWFSDLPGAGANNPTFRVYBTDAYSKIQDISTYFINLDD
LNKNKSTPFVFEYSFKDAYGITGDINPTTMSALLDKMKNNDTLFKKYIDYNTAFWNPQ
MPLGVYRGAQLCSMEYSDYPRYYSCLSKYTKSATRSLNIPLFSLFAIIYTELFLFLSF
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KRYSNSQAVEEIEKNTCNWYLDNNWYCNGAIEVSAWYFGWTFAVKLCHNLYMCASPSS
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DESSRRRSVPETPEESIRTVMLEKWNEIIFMNISEQLLVEALRLVKEERDGNIIDAQN
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                                                                                                                                  complement(join(11155. .12030,12072.
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8984..9175,9380..9520,9590..9715,9760.
                                                                                                 complement (join (11155.
                                                                                                                            /gene="ZK856
                                                                                                                                                                                                                       FRRTKIIPPPPMRQEIAPVTQQIMNCYINSIRKGDSBIGRQRQLSLCSKMBLEYNWTG
                                                                                                                                                                                                                                                                                                                                                   SKWVLHFQLFSDIHTRYKNSTYQHPKKKEKSPKNAILINLKNTLGGEKFTVEDVKQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphodiesterase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (gene="ZK856.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ZK856.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="ZK856.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ZK856.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILKTRKTYTLAQLTMELVEILKPLFIPNRKIIKEQIDWLIENKYMERRADDINTFVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MQFDEEWSKADPIVHALLHQKSVTPAAWQDLFYHVYKITSWVDD
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                                                              /gene="ZK856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7584. .7678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(6516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="SWISS-PROT:Q23639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Weak similarity with spingomyelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oin(6516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otein_id="CAA94852.1"
_xref="GI:3881806"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yk570c12.5
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yk570c12.3 comes
yk539d11.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yk310h9.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6596,7028. .7111,7164. .7379,7429. .7540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6596,7028. .7111,7164.
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197.3 comes from this gene

197.5 comes from this gene

18.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from this gene
from this gene
from this gene
from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7379,7429.
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RESULT 7
AC016944/c
                                                                                            ACCESSION
VERSION
                                                                      KEYWORDS
                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                             ORGANISM
                                                                                                                                                                                                                                                                                                        22923 AAGATTTCGAAAAAAGGAAATAACTTCGTGA 22953
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                                                                                                                                                                                                                                                                                                                                                         2 AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                158886 bp DNA
Homo sapiens chromosome 3 clone RP11-70P20,
11 unordered pieces.
                                                                    HTG;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                            AC016944
AC016944.14 GI:9929553
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                          sapiene
                                                                 HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q23640"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(12949. .13101,13147. .13350))
/gene="ZK856.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mvksvgcknlsldvkkaivagfeqgiptkmlalqiqrspstiwk
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rfqyenilettmrpmalqnvgrgfvpqqdndpkhtslhvrsmfqrrrvhlldmpsqsp
plnpienitetmrelerricgiirasnadakfnqlenamkaipmsvihklidsmprrcqavi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(25949. .26187,26233. .26457,26508. .26564,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:Q23642"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(12949. .13101,13147. .13350))
/gene="ZK856.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAVQKDRQGAICKGQCAPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WESKLFSCIYQYLSIL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ZK856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="CAA94855.1"/db_xref="GI:3881809"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="CAA94853.2"
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/db_xref="SPTREMBL:Q23636"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCECRLRROFKDFEKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SPTREMBL:Q23641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                      66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lement (join (25949. .26187, 26233. .26457, 26508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Digan-Rocha, S., Durbin, K.J., Ganesh, R., Gorrell, J.H., Gorrell, L.L., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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Consensus quality: 144562 bases at least Q40
Consensus quality: 152026 bases at least Q30
Consensus quality: 154719 bases at least Q20
Estimated insert size: 155752; sum-of-contigs estimation
Estimated insert size: 209830; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.3x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP11-70P20
Center Summary Statistics
Sequencing vector: M13; L08821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-FBB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced gi:12964402.
                                                                                                                                http://www.sanger.ac.uk/HGP/Chr13
RP11-418110 is from the library RPCI-11.2 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This sequence is the entire insert of clone RP11-418I10 The true left end of clone RP11-347N5 is at 72478 in this sequence. The true
                                                                  VECTOR: pBACe3.
                                                                                                 http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                     Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                         database can be found at
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/chromosome="3"
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157240: contig of 1391
157340: gap of unknown
158886: contig of 1546
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26800._.26832
/note="Sequence form overlapping clone bA307B20
(AL139802).Assembly confirmed by restriction digest data."
/note="Sequence from overlapping (AL356266).Assembly confirmed by 30906 c 29579 g 47018 t
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(AL356266).Assembly confirmed by restriction d
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(AL139802).Assembly confirmed by restriction digest."
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Caenorhabditis elegans
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Submitted (12-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is
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/db_xref="taxon:6239"
/clone="Y69A2R"
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Pred. No. 3.4e+02;
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Submitted (19-APR-2002)
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                                                                                                                                                                                                                                                                                                                                        Submitted (07-SBP-2001) Department of University, Genome Sequencing Center, Louis, MO 63110, USA 6 (bases 1 to 188616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-OCT-2000)
University, 4444 Forest
4 (bases 1 to 188616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology. The C. Science 282 (5396), 2012-2018 99069613
                                                                                                                    Submitted by:
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                                                                                                                                   University, Genome So
Louis, MO 63110, USA
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                                                                                                                                                      University,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ouis, MO 63110,
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Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
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                                                                                                                                                   2002) Department of Sequencing Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans
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REFERENCE AUTHORS TITLE

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NOTICE: This sequence may not be the entire insert of thi It may be shorter because we only sequence overlapping seconce, or longer because we provide a small overlap between neighboring submissions. **Bections**

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

For a graphical representation of this cosmid sequence and its analysis see: www.wormbase.org/db/seq/sequence?name=Y69A2AR;class=Sequence)

NEIGHBORING COSMID INFORMATION

cosmid is Y69A2AL, 200 ģ overlap; the ų cosmid 18 Y94H6A,

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the progra Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The program

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FEATURES
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9241. .9476,9528. .9852,9897. .10148)
/gene="Y69A2R.19"
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yk2495.3, yk2495.5, yk33d4.3, yk33d4.5, yk159f10.3,
yk159f10.5, yk251h10.5, yk352f7.5, yk356e6.3, yk356e6.5,
yk420b7.5, yk834g06.3"
                                                                                                                                                  TATEVKAVVESIQKSGSLEKFKQILLLLQKTFADVDGNILKTVILGGIKARITKIGDS
TFGDFIREELKHTCLKAQEEQSRKLSQAIQATQSLEKLDEKKLEVGSAASAVSSFA
KDLATIKSIBETMKERAKGUSTDLAUGHADAKKKUSDVGQSVSSLQDASELIELESIK
KDLATIKSIBETMKERAKGUSTDLAUGHADAKKKUSDVGQSVSSLQDASELIELESIK
KELKGFGPEIDGYIKAVKSPEDRKAIETQWGNHHSDMASLESGLKAAKGFVDKIDVSKA
KTMSDVGTTELANLKDLEDVKINALEKIKALDALIKALPPEKRKAATSDPKTVMEAAKS
TLEKLAALDLQFSNHKTQYQQAPAAFKAFHDFLAKFLVTTHSNSTGGSDSGISITLI
IIVGSILALIGYAVGIYGVRWYEKKKAAEQMEHEIVVMVXAQAYKSLBAAIIVLAS
LHVWGTQTSVSVEKSNAYLFKEKNREPLATFQNBFTAVEVKSDGTRIPIHAVINTS
PDVDGNTQKFIATQGPLFNTSDDFWTMVQFHKVETVMLQFVEKEEKCHEYPPVRT
GQIVDLERYKLKTVTQBQILGDSTSKRTIQVEDTSKEFTRTITHYQYTKSDEKCHEYPVRT
GGHAQCFDLMNNAKESKKPIVVHCSAGIGRTVSFIATQYIPSAVLANRTLYLQQAVAEL
DDGGATACTHERVKLTAVGGUSTSKRTIQVEDTSKEFTRTITHYQYTKARTQAVAEL
                                                                               complement (10637
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TDQLSRMNDKLKPIVSSSVQQTIAVFQVLVNEISLLSSDSAEMSSVMAELDKCSRTLP
MDDQRVVGVELMKHINSLKLSLSQFAEFKTSTILNSLEKEITSFQNSYKFSDLQDPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDSPLEPRDSHDPLDLSTPQELQDVGRVARQEQTYDVDTPSSVESLDIPSDTSNNAGR
VARQVAPSKSADYLNHTTLIAHIANGIALQAGLMKGSIPIDAAVSELLNFGSVKVSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mQHKMRFGQLLLLALFGVANGYREQENTISSSVRQEKINDNHLD
SPRSDGHELMENPLDFIASHDFSDFLDFHELQIAGRVARQDNNNDHLDTHRSSAGHEL
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                                                                                                        DGRKDVLKKLEADGEVRKAKQDEKKATTGIDEDLGGDRKKGGAECIAVDMEY"
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protein_id="AAK68563.2"
db_xref="GI:16604217"
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/protein_id="AAL00873.1"
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                                                                                                                              ldqrwcaIqtveqmywvqvgsvyrlskeknIdmkhykeqfemldgghkflylaqeqfk
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translation="MLALQIQRSPSTIWKVIKKYQTEKSVALRISXGRPRVTTHRMDR
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www.wormbase.org/db/seq/sequence?name=Y69A2AR.20;class=Se
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.wormbase.org/db/seq/sequence?name=Y69A2AR.21;class=Se
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                      graphical representation of this gene see:
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                      2 (bases 1 to 206320) Kaul, R.K., Olson, M.V., Haugen, E.D.
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10398 AAAGCTTTGAAAAAAAAAGAATAAATTAGTGA 10428
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 206320)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 3
AC093418 AC020638
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DRGLCGGGVHSSIVKEAKNILNNAGGDKEIRVVAIGDKSRAGLQRLYANSILLSGNEIGR
APPSFADASIAAKAILDSGYDFETGTILFNRFKTVVSYETSKLQILPLEAIKAKEALS
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/gene="Y59A2AR.18"
/note="for a graphical representation of this gene see:
/www.wormbase.org/db/seq/sequence?name=Y69A2AR.18a;class=S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTDKNNSDSDEDIESLINHETSLEAAAKARKRRLLAMKSKIHGI
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EKAIDSVDLAMLAPKKIDMDLKRDIESKLQKLERRTQKAVATIIRQRLAEGKGDLAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yk83e3.3, yk83e3.5, yk85f6.3, yk85f6.5, yk108f5.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYDSVDDDVLQSYSEYSLAQLIYYGMKESATSELPASKYLSLSVPFLHPLLFKLSLFR
RPNFPHFKSFLSPPKIRCFDLFFIFLCVTRCYSDTFB"
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yk27397.3, yk329a9.3, yk329a9.5, yk400a7.3, yk413a10.3,
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Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. HindIII SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt 11	Consensus quality: 206318 bases at least Q20 Insert size: 206320; sum-of-contigs Quality coverage: 6.7x in Q20 bases; sum-of-contigs Overlapping Sequences: 5: Mapping in progress 3: RP11-70220 (UWGC:bc0189) AC016944 Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality -= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.	JOURNAL Submitted (23-AUG-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA REFERENCE 3 (bases 1 to 206320) AUTHORS Kail, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Seenphinmsachak, C., Phelps, K.A., Buckley, D., Raymond, C. and Haugen, E.D. Direct Submission Submitted (30-Apr-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Apr 30, 2002 this sequence version replaced gi:15281267. Center: University of Washington Genome Center Center Code: UWGC Web site: http://www.genome.washington.edu Draftling Center: Enformation Center clone name: chr-3 Center project name: chr-3 Center project name: chr-3 Center project name: R11-1035L22 (bc0587) Sequencing vector: plasmid; 44% of reads chemistry: Dye-terminator Ef; 33% of reads chemistry: Dye-terminator Eig Dye; 54% of reads Assembly program: Phrap; vergion 0.990319 Consensus quality: 206129 bases at least Q40 Consensus quality: 206299 bases at least Q40
1786 	3968 2608 2437 941 1001 4280 5303 355 4289 2260 2962 3370	512 449 449 2576 2576 763 14581 1164 511 1164 233 5383 5383 5383 5383 6272
<pre><800 1820 9486 2251 5101 5101 1369 <800 5101</pre>	3976 2583 2435 924 997 4199 5502 <800 4497 2251 2900 3384	
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389 4720 4720 372 372 4480 1783 	76 3635 83 6367 83 6367 35 113 24 4916 97 2479 99 16772 99 16772 00 2964 00 6115 00 6115 00 395 5879	
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as LOCUS runs of N, but the exact sizes of the gaps are unknown.	Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, WO 63108, USA On Mar 1, 1999 this sequence: version replaced gi: 4263456.	to 299081)	1 (bases 1 to 299081) Waterston, R.H. Waterston, R.H. ORIGIN The sequence of Caehorhabditis elegans clone	Caenorhabditis elegans. Caenorhabditis elegans JOURNA. Caenorhabditis elegans FEATURES Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida; Eukaryota; Rhabditidae; Peloderinae; Caenorhabditis. Sou	 ACQU6892 299081 bp DNA linear HTG 26-FEB-1999 ORGANIS Caenorhabditis elegans clone Y69A2, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces. REFERENCE	ACCESSION VERSION	ARGGSTTCGAAATAAAGGAATAAATTCGTGA 32 AROLS	Match 66.9%; Score 21.4; DB 9; Length 206320; Db 3 Local Similarity 80.6%; Pred. No. 3.3e+02; les 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	1492 1492 2135 2093 23 <800 Qy	1967 1191 ,1152 2197 2175	1444 1369 1338 1405 11498 10912 Que	1547 1651 1769 1701 881 888 BASE COUNT. ORIGIN	3825 3775 152 <800 5303 5230	322 6204 4313 4302 1681 1641 FEATURES	3776 3775 5859 5914 1924 1892	5645 5502 313 <800 13161 12910	1837 1820 1781 1701 3311 3326	2866 2900 2779 2767 308 <800	6644 6536 2758 2767 4845 4679	747 769 1545 1568 6731 6650	2880 2900 685 <800 2872 2903	47 <800 1437 1511 1572 1541	767 769 1729 1701 3436 3661	7336 7313 1972 2093 256 <800
.14 192/c AR020892 1567 bp DNA TION Sequence 100 from patent US 5789214.	5 GGTTCGAAATAAAGGAATAAATTCGTGA 32 	Query Match 66.2%; Score 21.2; DB 6; Best Local Similarity 82.1%; Pred. No. 7.1e+02; Matches 23; Conservative 1; Mismatches 4	OUNT 469 a 313 c 298 g 477 t	Patent: US I I	Unknown. Unknown. Unclassified. Unclassified. 1 (bases 1 to 1567)	AR016866 AR016866.1 GI:3973143			2 AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32	Local Similarity 80.6%; Pred. No. 3.1 hes 25; Conservative 0; Mismatches	ch 66.9%;	96473 a	/organism="Caenorhabditis elega /db_xref="Caxon:6239" //lb	rce .	* 216838 216851 * 216852 299081	gap of unknown contig of 5938	122086: gap of unknown 157435: contig of 3534	77806: gap of unknown 122072: contig of 4426	45694: gap of unknown 77792: contig of 3209	45680: contig of 1535		16968: contig of 9786		3087: contig of 3087

linear

PAT 05-DEC-1998

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* This record will be updated with the finished sequence * as soon as it is available and the accession number will
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1 (bases 1 to 1567)

1 (bases 1 to 1567)

Ryals J.A., Alexander, D.C., Goodman, R.M. and Ward, B.R. Method of protecting plants from comycete pathogens Patent: US 58:56154-A 100 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

(bases 1 to 1567)

(bases 1 to 1567)

Ryals, J.A., Friedrich, L.B., Uknes, S.J. and Ward, E.R.

Rethod of inducing gene transcription in a plant

Patent: US 5789214-A 100 04-AUG-1998;
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Sequence 100 from patent US 5856154.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	22:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
	24:	/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
ed. No	o. is treater	ed. No. is the number of results predicted by chance to have a ore greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

eco:

Result	Score	Query Match	% Query Match Length DB ID	₽.	ID	Description
	32	100.0	32	21	AAA96852	Guide desoxynucleo
ი 2	21.2	66.2		20	AAV62796	Tobacco SAR CHX in
c 3	21.2	66.2		20	AAV81680	Tobacco protein-sy
0	21	65.6		21	AAZ46404	Penicillium funicu
c 5	20.8	65.0		22	AAH54098	S. epidermidis gen
о 6	20.8	65.0		22	AAH54877	S. epidermidis gen
c 7	20.8	65.0	3463	22	AAH54633	S. epidermidis gen
ი 8	20.2	63.1		23	ABL23374	Drosophila melanog
9	20	62.5		22	AAF23810	Escherichia coli s

ALIGNMENTS

RESULT 1 AAA96852

AAA96852 standard; DNA; 32 BP

AAA96852;

19-FEB-2001 (first entry)

Guide desoxynucleotide building block G4.

promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; ss.

Synthetic.

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370.

29-MAR-1999; 99FR-0003925.

(MERI-) MERISTEM THERAPEUTICS.

Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises

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RESULT 2
AAV62796/c
ID AAV62796 standard; cDNA; 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrrxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a guide desoxynucleotide building block, which was used to link directional desoxynucleotide building blocks during construction of chimeric promoters of the invention. The specification describes chimeric expression promoters. These chimeric promoters construction describes chimeric expression promoters. These from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter are derived from intergenic regions. The chimeric promoters are derived from intergenic regions. The chimeric promoters are useful for producing transcenic regions.
                  The method is for isolating a chemically regulatable DNA promoter fragment from the 5' flanking region of a chemically regulatable gene a plant tissue. The method allows isolation of sequences which will be useful for the controlled expression of genes, under the control of a
                                                                                                                                                                                                                                                                                                                                 31-MAY-1995;
                                                                 resistance (SAR) cyclohexamide (CHX) independent.
This gene can be isolated using the method of the invention.
The method is for isolating a chemically regulatable DNA pro
                                                                                                                                                Example 40A; Column 255-258; 175pp; English
                                                                                                                                                                             Isolating chemically regulatable DNA sequences in plants - useful for chemically controlling expression in transformed plants
                                                                                                                                                                                                                                                                 Harms C,
                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana acuminata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemically regulatable DNA promoter; expression control; herbicide tolerance; systemic acquired resistance gene; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco SAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with
      non-coding
                                                                                                    This sequence re-
resistance (SAR)
                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence from
                                                                                                                                                                                                                                                                                                 (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ence from promoter comprising vascular expression region replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGGTTCGAAATAAAGGAATAAATTCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGGGTTCGAAATAAAGGAATAAATTCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
                                                                                                                                                                                                                                                                 Ryals JA;
      regulatable sequence. This is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHX independent gene clone 11.3.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 14 A; 3 C; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                  represents a clone of the tobacco
                                                                                                                                                                                                                                                                                                                                 95US-0456262.
                                                                                                                                                                                                                                                                                                                                                                95US-0456262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 21;
Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                  systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
      plants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; pesticide;
                                                                                                                  acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Moyer MB,

Payne GB,

Ryals JA,

Ward ER;

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RESULT 3
AAV81680/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC chemical regulator, the regulator being applied before or with the CC chemical regulator, the regulator being applied before or with the CC chemical regulator, the regulator being applied before or with the CC cheight or pesticide to give optimal tolerance. The promoter fragment CC is useful for controlling sequences which encode traits such as CC height, shape, development, male or female sterility, and the ability CC of the plant to withstand cold, heat, salt and drought. The chemical CC industrion of the promoter allows the regulation of production of CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners, CC industrial feedstocks, antimicrobials and pharmaceuticals, by the object of the second cold, whose biosynthesis is controlled CC by endogenous or foreign genes. The method allows control over the time CC contract of gene expression either throughout the whole plant, or in CC localized tissues, to achieve e.g. fungal or insect resistance by for CC contract controlling the chemical regulator. Controlling the Cdevelopmental processes by the application of a regulating chemical in CC e.g. the commercial production of cultivated crops allows processes such as germination, flower formation and fruit ripening to be synchronised at CC and the control of cultivated crops allows processes such control in the control of cultivated crops allows processes such control in the control of cultivated crops allows processes such control in the control control in the control con
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Best Local :
                                                                                                                                                                                                                   20-OCT-1989;
07-SEP-1990;
21-DEC-1990;
01-APR-1991;
27-SEP-1991;
                                                                                                                                                                               06-MAR-1992;
06-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                08-MAR-1988;
06-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulation; transcription; plant tissue; chimeric construction; PR; pathogenesis-related protein; anti-pathogenic; transgenic plant; beta-1,3-glucanase activity; pest resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV81680 standard; DNA; 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1567 BP; 469 A; 313 C; 298 G; 477 T; 10
                                                         (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                          20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                               24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5847258-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tobacco protein-synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV81680
                                                                                                                                       L2-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                               93US-0042847.
93US-0045957.
93US-0093301.
94US-0181271.
                                                                                                                                                                                                                                                             89US-0368672.
89US-0425504.
90US-0580431.
90US-0632441.
                                                                                                                                                                               92US-0848506.
92US-0973197.
                                                                                                                                                                                                                       91US-0678378.
91US-0768122.
                                                                                                                                                                                                                                                                                                                                                                  89US-0305566
                                                                                                                                                                                                                                                                                                                                                                                      95US-0457364
88US-0165667
                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0457364.
                                                                                               3-0093301.
3-0181271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.2%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             independent gene p11.3.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 50;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
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#XEEX#X5505050505050
RESULT 4
AAZ46404/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a DNA molecule encoding a pathogenesis related (PR) protein having beta-1.3-glucanase activity selected from PR-2, PR-2', PR-2'', PR-N, PR-0 and PR-0'. Also described are: (1) a chimeric gene comprising the above DNA molecule linked to a heterologous promoter; (ii) a vector containing the chimeric gene; (iv) a transgenic plant containing the chimeric gene; die chimeric gene; and (v) a seed from the transgenic plant to DNA molecule is used to produce transgenic plants with enhanced disease or pest resistance. The present sequence represents a tobacco
                                                                                                          06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzyme mixture; xylanase; beta-glucanase cellulase; feruloyl esterase; digestibility; vegetable; cereal; livestock; supplement; nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ46404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ46404 standard; DNA; 2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1567 BP; 469 A; 313 C; 298 G; 477 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-synthesis independent gene pll.3.8 from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059180/05
           Sabatier A,
                                                                                                                                      11-NOV-1999.
                                                                                                                                                                 W09957325-A2
                                                                                                                                                                                                                                                                                                         Sgo
                                                                                                                                                                                                                                                                                                                                                                                            Penicillium funiculosum.
                                                                                                                                                                                                                                                                                                                                                                                                                   digestibility; vegetable; cereal; livestock; supplement; nutrition; food; energy; cell wall; phosphorus; usage; excretion; ammonia release; battery; intensive; agriculture; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penicillium
                                                                                06-MAY-1998;
                                                                                                                                                                                                                                                                 intron
                                       (RHON ) RHONE-POULENC ANIMAL NUTRITION SA. (RHOD ) RHODIA CHIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 GGTTCTANATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding pathogenesis-related glucanase proteins - useful for ducing transgenic plants with enhanced disease or pest resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           funiculosum xylanase C DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column 249-252; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
             Fish NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                98EP-0401101.
                                                                                                          99WO-IB00856.
                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                    number= 1
                                                                                                                                                                                                                                                                                                                                   *tag= a
                                                                                                                                                                                                                    643..2898
                                                                                                                                                                                                                                                                            product= "Penicillium funiculosum xylanase
                                                                                                                                                                                                                                                                                                                       number= 1
                                                                                                                                                                                                                                                                589..1642
                                                                                                                                                                                                                                                                                                       317..2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.2%;
82.1%;
           Haigh NP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.2;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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AAH54098/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xylanases, beta-glucanase cellulases or feruloyl esterases. These enzymes improve the digestibility of vegetable sources (particularly cereals). Supplementation of the diets of pigs with xylanase increased the energy digestibility by at least 6% as compared to unsupplemented diets, indicating that the enzyme is increasing the breakdown of cell walls (particularly those of wheat), causing the release of additional food energy in the small intestine. The enzyme mixture from the novel penicillium funiculosum strain is used for feeding livestock, especially by improving the digestibility of cereals such as wheat, rye, barley, triticale, oat, rice, oil seeds such as soya, sunflower, rapeseed, and cereal by-products such as wheat bran. The novel enzymes decrease by-products such as wheat bran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents Penicillium funiculosum genomic DNA encoding xylanase C. The invention relates to a novel strain of Penicillium funiculosum, deposited under the Budapest treaty as IMI No. 378536,
                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                               S. epidermidis genomic polynucleotide sequence SEQ ID NO:3462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2283 ĠĠĠŤŤTAĀĀĀŤĀĀĀTĀĀĀŤĀĀŤĀČŤŤĠĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2898 BP; 802 A; 705 C; 597 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel enzymes decrease phosphorus excretion, increase digestive use of phosphorus, improve amino acid digestibility and reduce the ammos in the air of animal batteries used in intensive agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               digestibility for farm animals
                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                       09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH54098 standard; DNA; 3103 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and an enzyme mixture obtainable from this strain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Penicillium funiculosum, useful for increasing the feed
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                            Claim 8; Page 1028-1030; 2188pp; English.
                                                                                                                  WPI; 2001-316495/33.
                                                                                                                                                  Kimmerly WJ;
                                                                                                                                                                                                                     09-NOV-1999;
                                                                                                                                                                                                                                                                                           17-MAY-2001.
                                                                                                                                                                                                                                                                                                                           WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                           vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH54098;
                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GGGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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Pred. No.
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

(II), gi

given in AAG81454 to AAG83120, from Staphylococcus epidermidis

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RESULT 6
AAH54877/c
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Matches · 25
AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and, (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.
                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. epidermidis genomic polynucleotide sequence SEQ ID NO:4241.
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                                                                                                                                                                                                                                                                                              Claim 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimmerly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination;
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. 25; Conser
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                                                                                                                                                                                                                                                                                       Page 1961-1962; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 3438 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endocarditis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP LTD
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78.1%;
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Pred. No. 75;
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RESULT 7
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in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 44 no sequences are present for SEQ ID NO:4465 to 4464.
                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. epidermidis genomic polynucleotide sequence SEQ ID NO:3997
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                                                                                                                                                                                                                                                                                                                Claim 8; Page 1670-1671; 2188pp;
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                                                                                                                                                                                                                                  AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                                                                                                                            AAH52304 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
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78.1%;
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RESULT 8
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                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL23374
                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 21595; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE )
                                σ
                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences are
GTTCGAAATAAAGGAATAAATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATTGTTTGAAATAAATAAAAAGATTCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGGTTCGAAATAAAGGAATAAATTCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
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25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 2894
                                                                                                                                                                           2894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster genomic polynucleotide SEQ ID NO 21595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-191637P
2000US-0614150
                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 1157 A; 549 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                         698 A; 699 C; 752
                                                                                               63.1%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.0%;
78.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent
for elucidating ce
                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred. No. 76;
0; Mismatches
                                                                                                  Score 20.2; DB 23
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 G; 1116 T; 0 other;
                                                                                                                                                                         9
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                                                                                                                                                                         745 T; 0 other;
                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nt for detecting 1000 or more cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              띪
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                           2894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                           Gaps
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WO200077247-A1 Escherichia

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AAF23609
AAF23609
ID AAF7
XX AAF7
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AAF23810
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                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                     sample.
saliva,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                           Escherichia
                                                                                                                   AAF23809;
                                                                                                                                       AAF23809 standard; DNA; 1583
                                                                                                                                                                                                                                                                                 Sequence 360
                                                                                                                                                                                                                                                                                                             useful for developing probes or primers that can be used to detect E. coli serotypes 0157:H7, 0157:NM or 055:H7, as well as developing nucleic acid based assays to detect E. coli serotypes in a biological sample. The sample can be a clinical (e.g. blood, urine, serum, tears
                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               and 055:
                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA markers useful for based assays for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112229/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2000; 2000WO-CA00716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200077247-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; serotype-specific marker; O157:H7; serotype detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF23810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF23810 standard; DNA; 360
                                         serotype
                                                    Escherichia
                                                                                               22-MAR-2001
                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                     The present
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                                                                                                                                                                                              GGTTGTGAATAATGGAATAAATTCTTGA
                                                                                                                                                                                                           GGTTCGAAATAAAGGAATAAATTCGTGA
                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV GUELPH.
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                      faeces
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                                           detection;
                                                                          coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¤,
                                                    coli;
                                                                                                                                                                                                                                                                                                                                                         sequence is a part of a novel DNA marker specific coli serotypes O157:H7, O157:NM and O55:H7. The DN
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli serotype-specific marker fragment.
                                                                                                                                                                                                                                                                                B₽;
                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                     or tissues),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0139260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li J;
                                                                                                                                                                                                                                                                                 94
                                                                        serotype-specific
                                                   serotype-specific
                                                                                                                                                                                                                                                                                A; 91 C;
                                                                                               entry)
                                                                                                                                                                                                                                                 62.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                         developing probes,
Escherichia coli se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒP
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                                                                                                                                                                                                                                                                                                   food, water or
                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                78 G;
                                                                                                                                       ВP
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                              186
                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                 97
                                                                          1583
                                                     marker;
                                                                                                                                                                                                                                                                                 <u>;</u>
                                                                                                                                                                                                                                                 1.3e+02
                                                                          ģ
                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                                      environmental sample
                                                                           marker.
                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                          serotypes
                                                     0157:H7;
                                                                                                                                                                                                                                                                                                                                                                                                                                   primers
                                                                                                                                                                                                                                                           Length 360;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O157:NM; O55:H7;
                                                     O157:NM; O55:H7;
                                                                                                                                                                                                                                                                                                                                                                                                                         and nucleic
0157:H7, 015
                                                                                                                                                                                                                                                                                                                                                       The DNA marker
                                                                                                                                                                                                                                                                                                                 serum, tears
                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                       eic acid
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18

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RESULT 11
AAD17286
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a novel DNA marker specific for Escherichia coli serotypes 0157:H7, 0157:NM and 055:H7. The DNA marker is useful for developing probes or primers that set to detect E. coli serotype: 0157:H7, 0157:NM or 055:H7, as well as developing nucleic acid based assays to detect E. coli serotypes in a biological sample. The sample can be a clinical (e.g. blood, urine, serum, tears, saliva, faeces or
                                                                                                                                            15-FEB-2000; 2000EP-0200506.
                                                                                                                                                                                                                                                                                                         29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA markers useful for based assays for detecting
                        Example
                                          An improved multiplex ligation-dependent amplification method for detecting specific single stranded target nucleic acids in sample
                                                                                                   Schouten
                                                                                                                                                                  15-FEB-2001; 2001WO-EP01739.
                                                                                                                                                                                       23-AUG-2001.
                                                                                                                                                                                                            WO200161033-A2
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                    Human ribosomal protein S24 probe #2 for MLPA assay
                                                                                                                                                                                                                                                                                                                                                   AAD17286 standard; DNA; 49 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues), food, water or environmental sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           based assays
and OS5:H7 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112229/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2000
                                                                                                                       (SCHO/) SCHOUTEN J P.
                                                                                                                                                                                                                                                                                                                                                                                                         159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYGU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                             2001-550053/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                         GGTTGTGAATAATGGAATAAATTCTTGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                    multiplex ligation-dependent amplification; amplicon; probe; nucleotide polymorphism; ribosomal protein; S24; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIND
                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 1;
                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUELPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-CA00716
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9908-0139260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li J;
                       151; 158pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 A; 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developing probes, primers
Escherichia coli serotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>.
                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1583;
                                             acids in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and nucleic acid O157:H7, O157:NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sample can
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serotypes
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cc amplification method for detecting specific single stranded target conucleic acids in samples using a plurality of probe sets comprising at cleast 2 probes. Each probe comprises a target specific region and a conn-complementary region comprising a primer binding site. The probes conplished by a primer set. The method is used for detecting a nucleotide polymorphism, especially a single nucleotide polymorphism; detecting multiple single stranded target nucleic acid sequences (through the cetection of multiple amplicons); determining the absolute or relative abundance of multiple single stranded nucleic acids in a sample; and detection of a break point region in rearranged nucleic acids. By using a femtomolar amount of the probes, a large number of different probe sets can be used to simultaneously detect and quantify a corresponding clarge number of target sequences with high specificity. The present DNA sequence is human ribosomal protein S24 probe which is used in a multiplex ligatable probe amplification (MLPA) assay.
  Sequence
  49
B₽;
  19
A; 7 C; 14 G; 9 T; 0 other;
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Matches
                           Query Match
Best Local
   N
AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
                   Similarity 77., 24; Conservative
                           61.9%;
                  Score 19.8; D
Pred. No. 1.3e
0; Mismatches
                   0,
                  ..3e+02;
7;
                                    BB
                                    22;
                                    Length
                    Indels
                                     49;
                    0
                    Gaps
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밁 á

10

AAGGGTTGGAAAATAAGACAGAAATTCGGGA 40

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RESULT 12
ABV60512
                                           Human; prostate pharmacogenomic
WO200160860-A2
                                                                                 Human prostate expression marker cDNA 60503
                                                                                                                                  ABV60512;
                                                                                                                                                          ABV60512 standard; cDNA;
                      Homo sapiens.
                                                                                                           13-SEP-2002
                                                                                                         (first entry
                                               cancer;
                                             cytostatic;
gene; ss.
                                                                                                                                                          241
                                                                                                                                                          ВР
                                                           carcinogen;
                                                           pharmacodyanamic
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marker;

17-FEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P. 20-FEB-2001; 2001WO-US05171. 23-AUG-2001.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

Schlegel ₽, Endege Š Monahan

WPI; 2001-662795/76

Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer

Page 11524; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer; monitoring the progression of prostate in a patient;

The invention

relates to an

improved multiplex ligation-dependent

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RESULT 13
ABA46292/c
ID ABA46292 standard; DNA; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                  The invention relates to a spatially-addressable set of single exornucleic acid probes for measuring gene expression in a sample derive from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. General management of the service of the microarray of the service of the microarray of the probes are useful for gene discovery, and for encode proteins of the microarray of the service of the microarray of the probes of the microarray of gene discovery, and for encode proteins predisposition and/or prognosing breast disease. General management of the probes of the microarray of the probes of the microarray of general discovery.
                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient; (I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cell single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA46292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assessing the ef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATAAAGGAATTAATTCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                   SEQ ID NO 4987; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the efficacy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.
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     is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a test compound to inhibit prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 G;
for assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뮸
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe #4987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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  of chemical
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                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                       derived
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Query Match Best Local Similarity

61.9%; 77.4%;

Score 19.8; DB 22 Pred. No. 1.6e+02;

DB 22;

Length 468;

Sequence 468

BP; 110 A; 126 C; 52 G; 180

T; 0 other;

The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid

Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form from WIPO at ftp.wipo.int/pub/published_pct_sequences.

tormat

directly

O.

ftp.wipo.int/pub/published_pct_sequences

fetal liver. The present probe of the invention.

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RESULT 14
ABA56837/c
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Best Local :
                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207446.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023659.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                   Penn
                                                                                                                                    Claim 1;
                                                                                                                                                          analyzing
                                                                                                                                                                   Human genome-derived single exon nucleic
                                                                                                                                                                                            WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human foetal liver single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA56837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA56837 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGGAGAGAAATAAAGGAAAAAATGAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIPO
                                                                                                                                                                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetal
                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                    SEQ
                                                                                                                                                          gene
                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                    ID'NO 5142; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 110 A; 126 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver;
                                                                                                                                                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                   Chen
                                                                                                                                                           in human fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression; single exon nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid probe #5142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 G; 180 T; 0 other;
                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                    acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Job time : 65.2356 secs

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RESULT 15
ABA26466/c
ID ABA26466 standard; DNA; 468
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                                                      Matches
                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                           Sequence 468 BP; 110 A; 126 C; 52 G; 180 T; 0 other;
                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 4932; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human hearts -  \\
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2002
                                                                                                                                                                                 congenital heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #4932 for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
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230 AATGGAGAGAATAAAGGAAAAATGAGTGA
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                                                   Score 19.8; DB 22; Length 468; Pred. No. 1.6e+02; 0; Mismatches 7; Indels 0
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Search completed: May 11, 2003, 03:16:51

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Perfect score:
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   441362 segs, 153338381 residues
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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(c) 1993 - 2003 Compugen Ltd
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Sequence 18,	Sequence 4,	Patent No. 54	Patent No. 52	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 8,	Sequence 6,	Sequence 7,	Sequence 20,
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ALIGNMENTS

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ATION NUMBER: DATE: 13-JAN. TICATION 435 FILICATION DATA ATION NUMBER: DATE: 16-JUL- FILICATION DATA ATION NUMBER: ATION NUMBER: DATE: 6-NOV- FILICATION DATA ATION NUMBER: ATION NUMBER: FILICATION DATA ATION NUMBER: DATE: 1-APR- TICATION NUMBER:	WIDENCES: 100 NDENCE ANDRESS: SEE: CIBA-GEIGY 7 Skyline Driv 17 Skyline Driv 18 York 19 York 19 YOR 19 YOR 19 YOR 10 SA 10532 READABLE FORM: TYPE: Floppy di REI IBM PC Compe RE: PSTEM: PC-ING RE: PSTEM: PS	Beck, Jam Duesing Friedrich Goodman, Ch Meins, Jr Montoya, Moyer, Ma Neuhaus, Payne, Ge Sperison, Stinson, Uknes, Sc Walliams, Williams, INVENTION:	ication ON: 18, John
US/08/181,271A -94 US 08/093,301 -1993 US 07/937,197 US 07/937,197 	rporation ble /MS-DOS se #1.0, Version	H. lie B. t M. ederick Marc B. stoph ey R. cally REGULATABLE EQUENCES AND USES	US/08181271A 1 A. Danny C.
	#1.25	AND ANTI-PATHOGENIC	

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 07/305,566

8-MAR-1988

US 07/165,667

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Best Local
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ENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Beck, James J.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 36,
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APPLICATION DATA:

US 07/368,672
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                          Harms, Christian
Meins, Jr., Frede
Montoya, Alice
                                                                Duesing,
Friedrich, Lesin
Taman, Robert M.
Montoya, A. Mary B.
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                                                                                                  Leslie B.
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PILING DATE: O.L.TA:
PRIOR APPLICATION NUMBER: US 07/678,378
APPLICATION INDEE: 1-APR-1991
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TITLE OF IN
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PRIOR APPLICATION NUMBER: US 07/425,504
PRILING DATE: 20-OCT 1989
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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PRIOR APPLICATION NUMBER: US 07/937,197
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                         FILING DATE: 20-OCT PRIOR APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                   FILING DATE: 24-MAR-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION UNMEER: US 07/165,667
FILING DATE: 8-MAR-1988
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ATTORNEY/AGENT INFORMATION:
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                                   APPLICATION NUMBER:
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: New York
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INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 Skyline Drive
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Stinson, Jeffrey
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                           UMBER: US 07/848,506
6-MAR-1992
                 12-APR-1993
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20-JUN-1989
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6-APR-1993
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                                                                   MBER: US 07/329,018
24-MAR-1989
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REG
TITLE OF INVENTION: DNA SEQUENCES
NUMBER OF SEQUENCES: 106
                            APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1567 base pair
                                                                                                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RBFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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APPLICATION NUMBER:
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: New York
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Payne, George B.
Payne, Christoph
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Friedrich, Les...
---Aman, Robert M.
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Meins, Jr., Frederick
Montoya, Alice
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Stinson, Jeffrey R.
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.2%;
US 07/678,378
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATABLE AND ANTI-PATHOGENIC CES AND USES THEREOF
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Sequence 100, App.

Application US/08449043

GENERAL INFORMATION: APPLICANT: Ryals, John A.

APPLICANT: APPLICANT: APPLICANT:

Duesing, Designed M.

Leslie B.

Beck, James J. Alexander, Danny C

Harms, Christian Meins, Jr., Fred Montoya, Alice

Frederick

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US-08-449-043-100/c
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                                                                                                                                                                                              US-08-444-803-100
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Best Local S
Matches 23
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
APPLICATION NUMBER: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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FILING DATE: 6-MAR-11
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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                                                             454 GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                             TOPOLOGY:
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FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
                                                                                             5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                              23;
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                            H: 1567 base pairs
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                            (919)541-8689
                                                                                                                                                                                                                               linear
                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                            single
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27-SEP-1991
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8-MAR-1988
                                                                                                                                             66.2%; Score 21.2;
82.1%; Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/045,957
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                                                                                                                              1; Mismatches
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                                                                                                                                                              DB 1;
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                                                                                                                              Gaps
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SOFTWARE: Patentin ReleacURRENT APPLICATION DATA:
APPLICATION UMBER: US/
FILING DATE: 24-MAY-199
CLASSIFICATION: 800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
APPLICATION NUMBER: 21-DEC-1990
                                                                                                                                                                                                                              APPLICATION NUMBER: PILING DATE: 27-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOP
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE: 7-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          APPLICATION NUMBER:
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DATE: 12-APR-1993
AGENT INFORMATION:
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Stinson, Jeffrey R.
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                                                                                                                                                                                                                                                                                                             UMBER: US 07/848,506
6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 07/425,504
20-OCT 1989
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                                                                                                                                                                                           7-SEP-1990
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                                                                          24-MAR-1989
                                                                                                                                   MBER: US 07/368,672
20-JUN-1989
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                                                                                          US 07/329,018
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US-08-456-265A-100/c
; Sequence 100, Application US/08456265A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (919)541-860 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/678,378
                                                                                                                                                                                                                                                                                          CLASSIFACTON DATA:
PRIOR APPLICATION NUMBER: US 08/181,271
PRIOR DATE: 13-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/456,265A
FILING DATE: 31-MAY-95
                                                                                                                                                                                                                                                                                 FILING DATE: 13-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                  FILING DATE: 8-MAR-1 PRIOR APPLICATION DATA:
                                                                              APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                  FILING DATE: 1-APR-1991 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 16-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                  APPLICATION NUMBER:
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                   APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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New York
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ucleic acid
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520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                     8-MAR-1988
                                                                                                                                                                                                                                                   JMBER: US 08/093,301
16-JUL-1993
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MBER: US 08/042,847
6-APR-1993
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
                                                                    US 07/165,667
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Pred. No. 7
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APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990

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Best Local (
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                                                                                                                                                                                                                                                                                                                                   equence 100, Application US/08455416
atent No. 5777200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                           APPLICANT
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE: 12-APK-110.
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
18,
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REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELENHONE: (919)541-8587
                TITLE OF INVENTION:
                                                  APPLICANT:
                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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APPLICATION NUMBER:
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Local Similarity 82.1%;
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IOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
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                                                                                                                                                                                                     Priedrich, Lest.
Aman, Robert M.
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Williams, Shericca C.
ENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC ENTION: DNA SEQUENCES AND USES THEREOF QUENCES: 106
                                                                                         Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                       Harms, Christian
Meins, Jr., Frederick
                                                                                                                                                                                                                                                                                  Alexander, Danny C.
                                                                            Uknes, Scott J.
                                                                                                                                                         Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                  Beck, James J
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                                                                                                                                          Neuhaus, Jean-Marc
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7-SEP-1990
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                                                            , Eric R.
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                                                                                                                                                                                                                                    Leslie B.
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Pred. No. 7.4;
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TELEFAX: (919)541-868
INFORMATION FOR SEQ ID NO:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pair
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FILING DATE: 8-MAR-1988
PRIOR APPLICATION UNMBER: US 08/042,847
FILING DATE: 6-APR-193
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 07/425,504
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APPLICATION NUMBER: US,
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                                                                                                                        REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: US 07/305,566
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 20-JUN
                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 7 Skyli
CITY: Hawthorne
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                                                                                                        TELEPHONE:
STRANDEDNESS
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             1567 base pairs
ucleic acid
                                                                                       (919)541-8689
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                                                                                                        (919)541-8614
                                                                                                                                                                                                                                                                                                                              20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                 JMBER: US 07/580,431
7-SEP-1990
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6-MAR-1992
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21-DEC-1990
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BR: S-19825/P1/CGC 1727
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                          APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
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                                                                                        APPLICATION NUMBER: US 07/305,566 FILING DATE: 6-FEB-1989
                                                                                                                                   APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
                                                                                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08 FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPB: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hawthorne 
: New York
                                                                                                                                                                               DATE:
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Stinson, Jeffrey R.
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Moyer, Mary B.
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Meins, Jr., Frederick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                           UMBER: US/08/455,244
31-MAY-1995
                                                                                                                                                                              6-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     George B.
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82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alice
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                                                                                                                                                                                                                                      US 08/093,301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christoph
                US 08/042,847
                                                                                                                                                                                             US 07/937,197
                                                                                                                                                                                                                                                                   08/181,271
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Pred. No. 7.
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SES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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US-08-455-244-100
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Patent No. 58
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                                                          APPLICANT
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                                                                                                                                 APPLICANT:
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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US 07/632,441
                                             APPLICANT
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/368,672
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                                                                                                                                                                                                                                                                                                                                                                                     GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 82.:
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
   INVENTION:
                                                                                                                                                                                                                                                                                                             Application US/08454876
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                                         Uknes, Scott
Ward, Eric R.
                                                                    Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                 Ryals, John A.
Alexander, Danny C.
                             Williams,
                                                                                                    Neuhaus, Jean-Marc
Payne, George B.
                                                                                                                                Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B
                                                                                                                                                                           Goodman, Robert
Harms, Christian
                                                                                                                                                                                        Friedrich, Leslie B. Goodman, Robert M.
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                                                                                                                                                                                                                                   Beck, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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7-SEP-1990
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                                                          Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.2%;
, Shericca C.
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                         John H.
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Pred. No. 7.4;
1; Mismatches
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NFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 13-JAN-9
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APPLICATION NUMBER: 1
FILING DATE: 20-JUN-
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FILING DATE: 27-SEP-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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ADDRESSEE: CIBA-GEIG
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                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                      NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0
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CITY: Hawthorne
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STRANDEDNESS:
                            ENGTH:
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               1567 base pairs
ucleic acid
                                                                                      (919)541-8689
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                                                                                                     (919)541-8614
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24-MAR-1989
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; MOLECULE TYPE: DNA (genomic) US-08-454-876-100
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US-08-457-364-100/c
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                                                                                                                                                         PILING DATE: 16-JUL-1993

PRIOR APPLICATION UNBER: US 07/937,197

PILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                               FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
                                                           FILING DATE: 6-FEB-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
              FILING DATE: 8-MAR-1988 PRIOR APPLICATION DATA:
                                                                                                               FILING DATE: 1-APR-1991 PRIOR APPLICATION DATA:
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FILING DATE: 31-MAY-1995
APPLICATION NUMBER:
                                                                                 APPLICATION NUMBER: US 07/305,566 FILING DATE: 6-FEB-1989
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                                               APPLICATION NUMBER:
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: New York
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5847258
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INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 Skyline Drive
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Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
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Friedrich, Les...
Aman, Robert M.
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Stinson, Jeffrey R.
Uknes, Scott J.
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Duesing, John H.
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Payne, George B
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                                               US 07/165,667
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US 08/042,847
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Pred. No. 7
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DATE:

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RESULT 10
US-08-456-262-100/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPAX: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       454 GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US (
FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991
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                                                                                                                                                                                                                                                                                             NO.
                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                          100,
                                                                                                                                                                                                                                                                            INFORMATION:
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5851766
                                                                                                                            Harms, L... Free Meins, Jr., Free Meins, Jr., Free Meins, Jr., Free Meins, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                           Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                               Duesing, John H. Friedrich, Lesli
                                                                                           Payne, George B.
                                                                                                                         Moyer, Mary B.
                                                                                                                                                                                    Goodman,
                                                                                                                                                                                                                               Alexander, Danny C.
Beck, James J.
                                                                                                                                                                                                                                                               Ryals, John A
                                                                                                         leuhaus,
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20-OCT 1989
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                              Eric R.
                                                                                                                                                                    Christian
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82.1%;
                                                                                                                                                                                    Robert M.
                                                                                                       Jean-Marc
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
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               Shericca C.
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                                                                                                                                                    Frederick
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Pred. No. 7.
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                  PRIDE AFFECTION NUMBER: US OB FILING DATE: 12-AFR-1993 ATTORNEY/AGENT INFORMATION: NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER.

PILING DATA: 07/165,667

APPLICATION NUMBER.
                                                                    REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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FILING DATE: 6-APR.193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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MEDIUM TYPE: Floppy
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                                                                                                      NAME: Elmer, James 9
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                 TELEPHONE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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New York
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                                     (919)541-8689
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                                                    (919)541-8614
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                                                                                                                                                                                                                                                                                                           MBER: US 07/580,431
7-SEP-1990
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                                                                                                                                                                                                       24-MAR-1989
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20-OCT 1989
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                                                                                                                                                                                                                          US 07/329,018
                                                                                                                                                                                                                                                                          US 07/368,672
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                                                                                                                                                                       US 08/045,957
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                                                                                                 36,129
                                                                                      S-19825/P1/CGC 1727
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; STRANDEDNESS: single TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-456-262-100
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Best Local Similarity 82.1
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT
APPLICANT
                                                                                                                                                      APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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APPLICANT
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               PRIOR APPLICATION DATA:
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                               APPLICATION NUMBER: FILING DATE: 6-FEB
                                                                                                                           APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                              APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
                                                                                                                                                                                                        APPLICATION NUMBER: 08, FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: CIBA-GEIGY Corporation
7 Skyline Drive
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Stinson, Jeffrey R.
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Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Montoya, Alice
Moyer, Mary B.
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harms, Christian
Meins, Jr., Frederick
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                               6-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             James J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jean-Marc
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82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shericca C
                                             US 07/305,566
                                                                                                                                                                                                                        08/181,271
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Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                       Version #1.25
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RESULT 12 US-08-455-736-100/c

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Sequence 100, Application US/08455736 Patent No. 5880328

GENERAL INFORMATION:

Ryals,

John A

PPLICANT

Duesing, u.... Duesing, Leslie b. Friedrich, Leslie b. Friedrich, Robert M.

Leslie B

Beck, James J.

Alexander, Danny C.

Harms, Christian Meins, Jr., Frederick Montoya, Alice Moyer, Mary B.

Neuhaus, Jean-Marc Payne, George B. Sperison, Christoph Stinson, Jeffrey R.

Uknes, L

Scott J.

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Matches
                                                                       Query Match
Best Local
                                                                                                                                                                                                                             INFORMATION FOR
                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTLING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/768,122
                                                                                                                                   TOPOLOGY: li
                                                                                                                                                                                                          FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-JUN-
PRIOR APPLICATION DATA:
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454 GGTTCTAAATAAAGGAATMAATTGATTA 427
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 12-APR
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                            5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                           23;
                                                                         Similarity
                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE:
                                                                                                                                                                                                                                      (919)541-8614
(919)541-8689
                                                                                                                                   linear.
): DNA (genomic)
                                                                                                                                                             single
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20-OCT 1989
                                                                       66.2%;
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                                                                       Score 21.2;
Pred. No. 7
                                                           Mismatches
                                                                                        DB 2;
                                                                                       Length 1567;
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                                                           Gaps
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TELEFAX: (919)541-8689
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-SEP-199:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 6-MAR-1: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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SEQUENCE CHARA
                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 20-JUI
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/181,271 FILING DATE: 13-JAN-1994 APPLICATION NUMBER: US 08/093,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
PILING DATE: 31-MAY-1995
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
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{ READABLE FORM:
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7 Skyline Drive
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6-NOV-1992
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6-MAR-1992
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20-JUN-1989
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                                                                                                                                                                                 US 08/045,957
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                                                                                        S-19825/P1/CGC 1727
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US-08-971-217-100/c
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Best Local Similarity
Matches 23; Conserv
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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PRIOR APPLICATION NUMBER: US 08/181,271
                                                                                                                                                                     APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                   PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 16-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 5942662artis Corporation STREET: 3054 Cornwallis Road, P.O. Box 12257 CITY: Research Triangle Park
                                                 FILING DATE:
                                                               APPLICATION NUMBER:
                                                                                                     APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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Harms, Christian
Friedrich, Leslie
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Ward, Eric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                   6-APR-1993
                                                                                                                                                                                                                                                                                                                                                               13-JAN-1994
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                                                                   US 08/042,847
                                                                                                                                                                                                                                                                            US 07/937,197
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    Mismatches

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Pred. No. 7
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US 07/425,504

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US-08-971-217-100
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                                                                                                                                                                                                                                                                                                                           ICERL INFORMATION:
ISNERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinshi, Hidean
                                                                                                                                                                                                                                                                                                                                                                                                                   09-350-600-100/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8587
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APPLICATION NUMBER: US 07/768,122
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                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 GGTTCTAAATAAAGGAATMAATTGATTA 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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   PPLICATION NUMBER:
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US 07/368,672
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                                                                                                                27709
                                                                                                                                                         Research Triangle Park
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82.1%;
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US/09/350,600
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Pred. No. 7.4;
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                                 #1.25
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TELEFAX: (919)541-8689
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/305,566 FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy PRIOR APPLICATION DATA: FILING DATE: 6-FEB-1989 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: FILING DATE: 14-NOV-PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: REFERENCE/DOCKET NUMBER: S-TELECOMMUNICATION INFORMATION: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0 PILING DATE: 14-NOV-1997 APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989 APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991 REGISTRATION NUMBER: APPLICATION NUMBER: US OF FILING DATE: 12-APR-1993 APPLICATION NUMBER: FILING DATE: 8-MAR-1988 APPLICATION NUMBER: US 07/165,667 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: STRANDEDNESS: TELEPHONE: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: ENGTH: nucleic DATE: 1567 base pairs 919) 541-8587 UMBER: US 07/381,443 18-JUL-1989 UMBER: US 07/937,197 6-NOV-1992 29-JUL-1988 17-MAY-1989 7-SEP-1990 JMBER: US 07/848,506 6-MAR-1992 6-APR-1993 31-MAY-1995 24-MAR-1989 20-JUN-1989 27-SEP-1991 21-DEC-1990 Timotny US 07/768,122 US 07/632,441 US 08/971,217 US 08/045,957 US 07/368,672 US 08/093,301 US 07/226,303 US 07/353,312 US 07/580,431 US 08/042,847 US 07/329,018 US 08/181,271 US 08/457,364 38,241 S-198250

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TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-702B-242
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US-09-453-702B-242/c
VS-09-453-702B-242/c
VS-09-452/c
VS-09
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Search completed: May 11, 2003, 03:08:10 Job time : 17.8321 secs
                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 20; DB 4; Length 31880; Best Local Similarity 82.1%; Pred. No. 30; Matches 23; Conservative 0; Mismatches 5; Indels
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Best Local Similarity 82.1%; Pred. No. 7.4;
Matches 23; Conservative 1; Mismatches
                                                                                                                                                                                28206 GGTTGTGAATAATGGAATAAATTCTTGA 28179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (608) 251-5000
. TELEPAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/110,955
FILING DATE: 04-DEC-1998
APPLICATION UMBER: 60/110,955
FILING DATE: 04-DEC-1998
APPLICATION INFORMATION:
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                                                                                                                                                                                                                                                               5 GGTTCGAAATAAAGGAATAAATTCGTGA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31880
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: WI
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB ID
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb htc: *
gb est3: *
gb est4: *
gb est5: *
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17 AQ449597
9 AV174753
17 BH147730
10 BB490355
17 AZ478586
13 BI327328
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 AQ449597 500002C12
AV174753 AV174753
BH147730 ENTQL82TR
BB490355 BB490355
AZ478586 1M0298G17
BI327328 AR077H09T
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AI059555 UI-R-C1-1		9	296	'n	20	2
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AZ198427 SP 1037 B		. 17	690	ω	0	5
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ALIGNMENTS

	source	FEATURES								•		COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AQ449597/c
organism="crypcosportain" parvum"	1728	Location/Qualifiers	Class: shotgun.	Seq primer: M13(-21) forward	For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html	Email: hyman@sequence.stanford.edu	Fax: 650 812 1975	Tel: 650 812 1972	855 California Avenue, Palo Alto, CA 94304, USA	Stanford University School of Medicine, Palo Alto	Stanford DNA Sequencing and Technology Center	Contact: Hyman, R. W.	Unpublished (1999)	Cryptosporidium parvum genome sequencing demonstration project	Hyman, R.W., Fung, E., Qin, F., Rowley, D. and Davis, R.W.	1 (bases 1 to 728)	Cryptosporidiidae; Cryptosporidium.	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;	Cryptosporidium parvum	Cryptosporidium parvum.	GSS.	AQ449597.1 GI:4578734	AQ449597	sequence.	2.x2 CpIOWAM13mp18gDNA1 Cryptosporidium parv	AQ449597 ' 728 bp DNA linear GSS 08-APR-1999	

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RESULT 2
AV174753/c
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ORIGIN
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukuniahi, Y., Funayama, T., Hara, A., Haydtsu, M., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramareu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 bp mRNA linear EST 07-JUL-1999
AV174753 Mus musculus C57BL/6J 8-day embryo Mus musculus cDNA clone
5730412A15, mRNA sequence.
                                                                                                                                                                                                                                                                                                    Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Trenmostabilization and thermoactivation of the synthesis of full length cDNA
(renc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV174753
AV174753.1 GI:5398849
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//clone lib="CpiOWAN13mp18gDNA1"
//lab host="E. coli DH125"
/not="Vector: M13mp18; Site_1: Hind III; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 1.5 and 3 kb. Adaptors (pGTGACTCA/CAAACCACTGAGTP) were ligated to the randomly sheared gDNA fragments and pAGCTCTTTG linkers were ligated to the Hind III-cleaved M13mp18 vector. The adaptor-containing inserts were annealed and ligated to the vector and transformed into E. coli strain DH125. Recombinant phagemid clones from the first plating of the library were randomly selected for sequence analysis using the M13(-21) forward primer."
76 a 133 C 91 9 328 t
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/clone_lib="Mus musculus C57BL/6J 8-day embryo"
/sex="mixed"
/dev_stage="8-day embryo"
                                                                                        /db_xref="taxon:10090"
/clone="5730412A15"
                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                          ocation/Qualifiers
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83.9%;
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Pred. No. 1.1e+03;
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BH147730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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        BASE COUNT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH147730 1016 bp DNA linear GSS 27-AUG-20 ENTQL82TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
Clones are derived from the Entamoeba
DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Entamoeba histolytica.
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          387
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/db_xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Paractical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
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a 39 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Entamoeba histolytica"
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81.2%;
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Pred. No. 3e+03;
0; Mismatches 6;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

URL:http://genome.gsc.riken.go.jp/

URL:http://genome.gsc.riken.go.jp/

Anninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

N., Okazaki,Y., Muramateu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length

CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

,Y. and Hayashizaki,Y.
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BB490355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                     system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
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nno,H., Aizawa,K.,
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                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.rtc.riken.go.jp) for
                             /dev_stāge="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2
                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                tissue_type="stomach"
                                                                                                                                                                     'clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                   clone="D530014M20"
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85.7%;
                                                                                                                                                                                                                              _xref="taxon:10090"
ite_1: Sall; Site_2: BamHI; cDNA library was
and sequenced in Mouse Genome Encyclopedia
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Pred. No. 2.5e+03;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                        days embryo
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn,D., Aoyagi,A., Baı
Islam,H., Longacre,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ478586 375 bp DNA linear 100298G17R Mouse 10kb plasmid UUGCIM library Mus
                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
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Plate: 0298 row: G column:
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                       quality sequence stop: 375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UUGC1M0298G17 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0298G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                       strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barber,M., Beacorn,T., Duval,B., Hamil,C.,S., Mahmoud,M., Meenen,E., Pedersen,T., ReillyR., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.4; DB 10
Pred. No. 4.4e+03;
0; Mismatches 6
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BI327328/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'CDNA adapter' etween the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 432)
Rink, A., Santchi, E.M. and Beattie, C.W.
Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 775 784 1705
Fax: 775 784 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pig.
Sue ecrofa
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AR077H09THYBH09S Porcine Thymus cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arink@cabnr.unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Rink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                        /note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI
                                                                                                                                                                                                                                                                  /clone_lib="Porcine Thymus cDNA library"
/tissue_type="Thymus"
/cell_type="mixed"
                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
                                                                                                                                                                                                        /dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 4.1e+03;
0; Mismatches 6
      of the EST.
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The adapter sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces Saccharomyces kluyveri, Kluyveromyces marxianus yar. marxianus, Pichia lactis var. lactis, Kluyveromyces marxianus yar. marxianus, Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1074)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS06XG0 1074 bp DNA 1
T3 end of clone XAXOAA00ZD12 of library XAXO
Fischia farinosa, genomic survey sequence.
                                                                                                                                                                                                                                                          5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL419686
AL419686.1 GI:12202864
                                                                                                                                                                                                                                                                                                                           angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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Saccharomycetales; Saccharomycetaceae; Pichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Montigny,J., Spehner,C., Souciet,J.,
Wincker,P., Artiguenave,F. and Potier,S.
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97 c 78 g
                                                                                   /clone_lib="XAX0AA"
/note="end : T3"
                                                                                                                                /db_xref="taxon:4920"
/clone="XAX0AA002D12"
                                                                                                                                                                                             organism="Pichia farinosa"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                           strain="CBS 7064"
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Length 1074;
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Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 502)
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HS_3218_B2_G02_T7 CIT Approved Human Ga
sapiens genomic clone Plate=3218 Col=4
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AQ100322.1 GI:3471351
GSS.
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HS_3054_A1_D06_MF CIT sapiens genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome Proc. Natl. Acad. Sci. U.S.A.
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Mammalia; Eutheria; Primates;
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(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tagged Connector
                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; BAC
E-Coli DH10B"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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                                                                                 GI:3625773
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78.1%;
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              Chordata;
Primates;
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Pred. No. 6.3e
0; Mismatches
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Approved Human Genomic Sperm Library D Homo
Plate=3054 Col=11 Row=G, DNA sequence.
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              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                          The Washington Univ. Nematode EST Project, 1999 Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
                                                                                                                                                                                                                                                                                                          McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Franklin, C., Tasgareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Sea
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceen.washington.edu
Sequence Tagged Connector
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
Mashington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI746889 546 bp mRNA linear EST rm33c01.y1 Meloidogyne arenaria egg pAMP1 v1 Chiapelli N Meloidogyne arenaria cDNA 5', mRNA sequence.
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Class: BAC ends
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High Throughput Sequencing Center
University of Washington
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                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                 Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
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llarity 78.1%;
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1 91 c 105 g 158 t 1 others
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/clone_lib="CIT Approved
/sex="male"
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db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        State University.
Seq primer: -40RP from Gibco
High quality sequence stop:
                                                                                                                                                                                        Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)
                                                                                                                                                                       Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
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/lab host="DH10B"
/lab host="DH10B"
/lab host="DH10B"
/note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1;
/note="Vector: pAMP1 (Gibco); Site_1! Not1; Site_2: Sal1;
/note="Vector: pAMP1 (Gibco); Site_1! Not1; Site_2: Sal1;
/note="Vector: pAMP1 (Chapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was made by using Dynabead oliversity, St. Louis. The
CDNA was made by using Dynabead oliversity from the
SMART PCR cDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nematodes were
provided by Dr. David Bird and Daniel Snyder of North
Carolina State University.".
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                                           /organism="Homo sapiens"
/db_xref="GDB:7524814"
/db_xref="taxon:9606"
/clone="RPCI-11-65J23"
/clone_lib="RPCI-11"
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/db_xref="taxon:6304"
/clone_lib="Meloidogyne arenaria
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78.1%;
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Pred. No. 5.4e+03;
0; Mismatches 7
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DEFINITION
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156 CAAGGGTTTGTGATAAAGGATTAATTTCATTA 187
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Other_GSSs: RPC111-64015.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fr
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fr
Research Genetice (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db xref="GDB:7524542"
/db_xref="taxon:9606"
/clone="RPCI-11-64015"
/clone_lib="RPCI-11"
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RPCI11 Human Male BAC Library"
72 c 130 g 165 t
                                                                                                                                                     /cell type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
109 c 122 g 211 t
                                                                                                                                                                                                               /sex="Male"
/cell_type='
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/note="Vector: pBACe3.6;
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RESULT 13 CNS045XL/c

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                                                                                                                                                                                                                                                                                                                                        CAATGGTTCTAACGAGAAGAATAAATTCTTGA 186
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Tetraodon
084H09 of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                    sequence.
AG144326
                                                                                                               Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-005E15.TJ.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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2 (bases 1 to 669)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Ronneau, L., Billault, A., Quetier, F., Saurin, W., Bernot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 669)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis
Tetraodon nigroviridis DNA sequence
                 BAC
                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                  AG144326.1
GSS.
                                                                                                                                                                                                                                   Pan troglodytes DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000)
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Tetraodon nigroviridis.
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GSS; genome survey seq
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            sequences
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/db xref="taxon:9983"
/clone="084H09"
/clone_11b="G"
/note="Genoscope sequence ID : C0BG084CD05SP1~end
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library G from Tetraodon ni
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78.1%;
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Catarrhini; Hominidae;
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ey sequence PUC-Ori end of
nigroviridis, genomic surv
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nigroviridis
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A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-912)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Totoki,Y., Mattanabe,H. and Sakaki,Y. Direct Submission
Submitted 'no ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV853564 Nori
                                                                                                                                                                                                                                                                                                                     Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T. Expressed genes in Ciona intestinalis Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis
                                                                                                                                                                                                                                                 Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
                                                                                                                                                                                                                                                                                   Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV853564.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of clone tracking errors.
                                                                                                                                                                                                                                     Tel: 81-75-753-4081
                                                                                                                                                                                                                                                                                                                                                                    Phlebobranchia; Cionidae;
1 (bases 1 to 768)
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R.Site 1 : EcoRI
R.Site 2 : EcoRI
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                                                                                                                                                                                                    satoh@ascidian.zool.kyoto-u.ac.
                            /organism="Ciona intestinalis"
/db xref="taxon:7719"
/clone="rcilv13h17"
/clone_lib="Nori Satoh unpublished cl/tissue_type="whole animal"
/dev_stage="larva"
/dev_stage="larva"
/note="Vector: pBluescript SK"
/note="Vector: JBluescript SK"
/note="Vector: JBluescript SK"
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/clone_lib="RPCI-43 Chimpanzee Male
/clone_133 c 125 g 205 t
                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:9598"
/clone="RP43-005E15.TJ"
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78.1%;
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Pred. No. 5e+03;
0; Mismatches
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Indels Length

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Gaps

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EST 08-NOV-2001 Ciona

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BAC

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cDNA library,

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Scoring table:
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              Score
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
              Match Length
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32
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(c) 1993 - 2003 Compugen Ltd
  10 US-09-864-761-4932
10 US-09-864-761-11326
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10 US-09-860-107-2125
10 US-09-880-107-2125
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10 US-09-815-242-6547
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10 US-09-315-124-1884
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US-10-114-170-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1567708
                                                                                                                                                                                                                                                                                                             Sequence 18, Appl
Sequence 242, App
Sequence 432, Ap
Sequence 11873, A
Sequence 11326, A
Sequence 2125, Ap
Sequence 1, Appli
Sequence 405, App
Sequence 405, App
Sequence 1, Appli
Sequence 405, Appl
Sequence 37, Appl
Sequence 2679, Ap
Sequence 128, Appl
Sequence 1884, Ap
Sequence 1884, Ap
Sequence 1804, Ap
Sequence 1809, A
Sequence 13097, A
Sequence 942, Appl
Sequence 942, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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RESULT 1 US-09-963-803-18 US-09-963-803-18 US-09-963-803-18 Publication No. US20030028922A1 Publication No. US2003002892A1 PUBLICANT: Merister Therapuetic expression promoters originating from commelina yellow ITILE REFERENCE: 184322042 CURRENT PILING DATE: 2001-09-26 PRIOR PILING DATE: 2001-09-26 PRIOR PILING DATE: 2000-10-05 PRIOR DATE: 2000-10-05 PRIOR PILING DATE: 2000-10-05 PRIOR DATE: 2000-10	20 18.2 56.9 1238 9 US-10-174-363-31 Sequence 31, Appl 22 18.2 56.9 1755 10 US-09-815-242-828 Sequence 4389, Ap 22 18.2 56.9 1861 10 US-09-822-830A-4 Sequence 268, Appl 25 18.2 56.9 2102 10 US-09-764-864-268 Sequence 268, Appl 25 18.2 56.9 5361 9 US-09-764-966-2 Sequence 27, Appli 26 18.2 56.9 8593 9 US-09-742-096-1 Sequence 135, Appl 27 18.2 56.9 8593 9 US-09-742-096-1 Sequence 135, Appl 27 18.2 56.9 8593 9 US-10-091-548-135 Sequence 135, Appl 27 18.2 56.9 8593 9 US-10-091-548-135 Sequence 135, Appl 27 18.2 56.9 35913 9 US-09-764-860-1196 Sequence 135, Appl 37 18.2 56.9 35913 9 US-09-764-860-1196 Sequence 135, Appl 37 18.2 56.9 35913 9 US-09-754-853A-3 Sequence 27, Appli 37 18.2 56.9 35913 9 US-09-754-853A-3 Sequence 370, Appli 38 18 56.2 431 9 US-09-754-853A-3 Sequence 370, Appli 38 18 56.2 431 9 US-09-784-853A-3 Sequence 3870, Appli 38 18 56.2 431 9 US-09-918-995-8666 Sequence 8370, Appli 38 18 56.2 11360 9 US-09-784-891-5508 Sequence 6506, Appli 56.2 11360 9 US-09-784-891-6508 Sequence 6506, Appli 56.2 55795 10 US-09-784-891-6508 Sequence 6506, Appli 56.2 55795 10 US-09-784-891-6508 Sequence 7415, Appli 66.2 56.2 56.2 56.2 56.2 56.2 56.2 56.2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                           Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Por
                                                                             FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28206 GGTTGTGAATAATGGAATAAATTCTTGA 28179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (608) 251-91
TELEPAX: (608) 251-91
INFORMATION FOR SEQ ID NO: 242:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * TOPOLOGY: linear MOLECULE TYPE: DNA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTCGAAATAAAGGAATAAATTCGTGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/114,170 FILING DATE: 01-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                      Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF INVENTION: NO. US20030023075A1el Sequences of E. coli 0157 R OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 31880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE: Quarles & Brady
TREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 3.1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31880;
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                                                                                                                                                                                                            Sequence 14873, Application US/09864761 Patent No. US20020048763A1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4932
LENGTH: 468
                                                                                                                                                                                           GENERAL INFORMATION:
                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          230 AATGGAGAGAAATAAAGGAAAAATGAGTGA 200
                                                                                                                                                                                                                                                                                                                                                                                 2 AAGGGTTCGAAATAAAGGAATAAATTCGTGA 32
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61.9%;
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DD IN HELLO, SIGNAL = 1.2
ED IN HELA, SIGNAL = 0.99
ED IN ETTAL LIVER, SIGNAL = 1.3
ED IN BT474, SIGNAL = 1.3
ED IN BRAIN, SIGNAL = 0.99
ED IN HEART, SIGNAL = 0.94
ED IN HEART, SIGNAL = 0.94
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Pred. No. 1.6e
0; Mismatches
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LUNG, SIGNAL = 1.2
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.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                    Sequence 11326, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 14873
LENGTH: 590
                                           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OP INVENTION: CENB EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                             APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
OTHER INFORMATION: MAP
                                                                                                                                                                                                                                                                                                                                                343
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
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                                                                                                                                                                                                                     INFORMATION:
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l, David K.
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NUMBER: US 09/608,408
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Pred. No. 2.4e+02;
D; Mismatches 6;
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RESULT 6
US-09-880-107-2125
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LENGTH: 466
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OTHER INFORMATION: I
OTHER INFORMATION: I
OTHER INFORMATION: I
                                             APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
                                                                                                                                       APPLICANT:
                                                                                                                                                                                    APPLICANT: Horne,
                                                                                                                                                                         APPLICANT:
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FEATURE:
OTHER INFORMATION: MAP TO AC005774.1
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FILING DATE: 2000-06-14
APPLICATION NUMBER: US 60/237,054
FILING DATE: 2000-10-02
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00669
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Scherf, Uwe
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75.0%;
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Pred. No. 2.7e+02;
0; Mismatches 8
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IN LUNG, SIGNAL = 0.65
IN BRAIN, SIGNAL = 0.76
IN ADULT LIVER, SIGNAL =
IN BONE MARROW, SIGNAL =
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RESULT 8
US-10-101-464A-405/c
Sequence 405, Application US/10101464A
Publication No. US20030046728A1
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Best Local Similarity 75.0%;
Matches 24; Conservative
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LENGTH: 38059
                                                                                                                                                                                       Matches
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APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684973 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCMBBErers, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                        Local Similarity
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CLASSIFICATION:
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                       Conservative
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75.0%;
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Pred. No. 8.4e+02;
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Pred. No. 6.4e+02;
D; Mismatches 8;
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RESULT 9
US-08-781-986A-37
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-405
               ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 9934 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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PRIOR FILING DATE: 2000-01-11
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STREET: """.
STREET: "".
STREET: "".
STREET: Maryland
""CA
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20850
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9410 Key West Avenue
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Pred. No. 3.8e+02
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US-08-781-986A-37
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US-09-815-242-6547
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                                                                                        Sequence 2679, Application US/09938842A Patent No. US20020160378A1
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Best Local Similarity
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                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ID NO 6547
ENGTH: 1524
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                                                                                                                                                                                                                             7 TTCGAAATAAAGGAATAAATTCGTG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
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                                                                  INFORMATION:
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Trawick, John D.
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76.7%;
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Pred. No. 5
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RESULT 12
US-09-070-927A-128
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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SEQ ID NO 2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                            INFORMATION FOR SEQ ID NO: 128
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1217 CAAGAGTTCGAAAGAGAGAATAAA 1241
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                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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Local Similarity 84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                 REFERENCE/DOCKET NUMBER: PB369 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                        NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
                                          LENGTH: .32768 base pairs
                                                                                                         TELEFAX: (301)
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                                                                                                                               (301)
                                                                                                           309-8512
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Pred. No. 6
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FOR

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Query Match
Best Local Similarity
Marches 22; Conserve
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US-09-764-847-1884/c
US-09-764-847-1884/c
Sequence 1884, Application US/09764847
Patent No. US20020132767A1
           RESULT 15
US-09-864-761-26009
; Sequence 26009, Application US/09864761
; Patent No. US20020048763A1
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                                                                                                                                                                                                               ; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1884
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US-10-092-154-1884/c
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NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1884
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1884
GENERAL
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Publication No. US20030054375A1
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                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.3

OTHER INFORMATION: SWISSPROT HIT: BE077941.1, EVALUE 7.00e-04

OTHER INFORMATION: SWISSPROT HIT: P10895, EVALUE 1.00e+00

OTHER INFORMATION: NT HIT: AL163268.2, EVALUE 7.00e-03
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CURRENT FILING DATE: 2001-05-23
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FILLING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00667
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SUMMARIES

RESULT 1 AX036742 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL		C C 443	c 40	C 36	C 33		c 27 c 28 29	C 25 25	c 22 23	c 19	176	ין נעני נטאי	10	087	σ ທ :	4 W 2 P	Result No.
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1 (bases 1 to 317)

Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating fromottle virus and cassava vein mosaic virus Patent: WO 0058485-A 3 05-OCT-2000;

MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);

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Sequence 3 from Patent WO0058485,
AX036737 GI:11226246
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/db_xref="taxon:32630"
/note="birectional desoxynucleotide building
/note="birectional desoxynucleotide building
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/note="promoter MPr1116"
L. .317
61 c 74 g 7:
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Pred. No. 5.2
0; Mismatches
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AX036740
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AX036738
AX036738.1
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Rance, I., Theisen, M. and Gruber, V.

Chimeric expression promoters originating fromottle virus and cassava vein mosaic virus patent: WO 0059485-A 4 05-OCT-2000;

MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); GRUBER VERONIQUE (FR)

Location/Qualifiers
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synthetic construct synthetic construct artificial sequences
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Similarity 100.0%; 1
58; Conservative 0;
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/db_xref="taxon:32630"
/note="promoter MPr1117"
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68 c 89 g 93
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Pred. No. 4e-12;
0; Mismatches 0;
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AX036758
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                                                                                                          Sequence 24
AX036758
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AX036759
    artificial sequences.

1 (bases 1 to 541)

Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating
                                                  synthetic construct
                                                                  synthetic construct.
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(bases 1 to 472)
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/db_xref="taxon:32630"
/note="promoter MPr1169"
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/db_xref="taxon:32630"
/note="promoter MPr1147"
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COUNT
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Sequence
AX036757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
        synthetic construct.
synthetic construct
artificial sequences.

1 (bases 1 to 392)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 21 05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 604)

Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                                                                                             Sequence 21 from AX036755
                                                                                                                                                                                                                                                                                              l Similarity
58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 24 05-OCT-2000;
                                                                                                                                  AX036755.1 GI:11226264
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MERISTEM THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1167"
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/db xref="taxon:32630"
/noTe="promoter MPr1168"
1. .541
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RANCE IANN (FR)
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4.2e-12;
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THEISEN MANFRED (FR)
                                     commelina yellow
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                                         artificial sequences.

1 (bases 1 to 462)

Rance,I., Theisen,M. and Gruber,V.

Ranceric expression promoters originating from mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 20 05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 393)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                    MERISTEM THERAPEUTICS (FR)
                                                                                                            synthetic construct
                                                                                                                    synthetic construct.
                                                                                                                                            AX036754.1 GI:11226263
                                                                                                                                                       Sequence 20 from Patent AX036754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct.
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AX036753
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Location/Qualifiers
1. .462
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/note="promoter MPr1164"
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Pred. No.
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o. 6.4e-11;
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5. 6.4e-11;
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                               IANN (FR) ;
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ORGANISM
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AX036756
LOCUS
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AX093047
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11 ACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT
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AX093047
AX093047.1 (
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Sequence 22
AX036756
AX036756.1
                                                                                                                  artificial sequences.

1 (bases 1 to 9285)
Gruber, V. and Comeau, D.
Synthetic vectors, transgenic plants containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 600)
Rance, I., Theisen, M. and Gruber, V.
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) , RANCE IANN (FR) ,
GRUBER VERONIQUE (FR)
                                                                                                                                                                                synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequences.
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                                                                                      for obtaining them Patent: WO 0118192-A 52 15-MAR-2001;
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                                                                            THERAPEUTICS
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="pMRT1336"
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1. 462
87 c 111 g 110
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/db_xref="taxon:32630"
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1. .600
111 c 147 g 15
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                                                                                                                                   complete genome; protease; reverse transcr
Commelina yellow mottle virus.
Commelina yellow mottle virus
Viruses; Retroid viruses; Caulimoviridae;
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1 (bases 1 to 15077)
Medberry,S.L., Lockhart,B.E. and Olszewski,N.E.
Properties of Commelina yellow mottle virus's complete DNA
                                                      Dept of Plant Biology, 22
Ave., St. Paul, MN 55108,
                                                                                Submitted (02-MAY-1990)
                                                                                                           Olszewski, N.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="pMRT1342 results from the replacement of the expression cassette ep355-gus-polyA355 from pMRT1335 by the expression cassette L5-gus-polyA358 isolated from pMRT1336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="synthetic construct"
/db_xref="taxon:32630"
/note="pMRT1342"
                                                                                                                                                                                           GI:59047
                                                                                                                                                                                                                      yellow mottle virus
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Pred. No. 9.4e-11;
                                                                   Olszewski N.B., University of 220 Biological Sciences Center,
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/GOGOD STEAT = 1
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/note="ORF 3,
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/proteIn_id="CAA37108.1"
/proteIn_id="CAA37108.1"
/db_xref="SWISS-PROT:P19200"
/db_xref="SWISS-PROT:P19200"
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KKLSEEVIVFTPEVKINLRDLAHNIHIIAHRVALGFKVIYLYLVDIIFPLLKNIQKSQ
KESSENLQSVLKIVKEQRRSLKQIEDOLSKVQSELAKLREDYLSRRPLSKQDVEELVV
RISBQPKFIEKQTEALTEELKLKVEBVAKLIHSFKGMVLN"
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/translation="MSNITESKGYKEALSVTNNYLAPAIGIGGATDVGLTGVTKOLNT
/TIYLLVAKITQOJIEDLOSTIKRLEERVQSLEKAKTPVVTQDPNPEIISKLSDIQISLAR
QRAVNPAISGVSNYTAPTIKKVDRILRVFKKFN"
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/protein_id="CAA37109.1"
/db_xref="GI:59049"
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/note="ORF 2"
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BASE COUNT ORIGIN Query Match Best Local Similarity Matches 47; Conserv variation variation old_sequence variation variation variation variation variation variation variation variation variation 2662 a 72.3%; Score 47; DB 14; Length 7489; ilarity 100.0%; Pred. No. 1.4e-07; Conservative 0; Mismatches 0; Indels /note="g in clone pCoYMV100" 1389 c 1577 g 1861 t /note="c in clone pCoYMV100" /note="additional t in pCoYMV100" 2672. .2674 /note="ccc was cc in [1]" /citation=[1] note="c in clone pCoYMV100" note="t in clone pCoYMV100" note="t in clone pCoYMV100" note="t in clone pCoYMV100" note="a in clone pCoYMV100" note="c in clone pCoYMV100" note="c in clone pCoYMV100" ٥,

Search completed: May 11, 2003, 06:04:51 Job time: 695.446 secs

7123 TATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATA 7169

16 TATCCGCCGTCATCAATGACATCACACAGTACTGAGGAGATGAATA 62

Gaps

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Result
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Maximum Match 100%
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Probe #3604 for ge	ABA25138	22	459	34.8	22.6	45
Human foetal liver	ABA55410	22	459	34.8	2	44
Human breast cell	ABA44936	22	459	34.8		3
. Pyrococcus abyssi	AAH41224	22	349980	35.1	2	42
Eucalyptus grandis	AAC55984	21	450	35.1	2	41
Human secreted pro	AAC59514	21	1809	35.4	23	
	AAH31993	22	470	35.7	23.2	39
Human cDNA differe	ABK83566	24	147724	36.0	23.4	38
	AAL21607	22	764	36.0	23.4	37
Human breast cance	AAL22984	22	570	36.0	23.4	36
Human breast cance	AAL12735	22	468	36.0	23.4	S S
Human breast cance	AAL14122	22	424	36.0	23.4	34
Human Tumour Endot	ABL92106	24	4168	36.3	23.6	ω ω
Drosophila melanog	ABL21738	23	2884	36.3	23.6	32
Drosophila melanog	ABL21739	23	1863	36.3	23.6	ω
Human ovarian tumo	AAH82620	22	385	36.3	23.6	30
Human ovarian PCR-	AAS24051	22	273	36.3	23.6	29
Modified adenovira	AAA59651	21	30115	36.6	23.8	28
DNA encoding novel	AAS84414	23	1467	36.6	23.8	27
Arabidopsis thalia	AAC37735	21	2320	36.9	24	
Human polynucleoti	AAI58954	22	1470	36.9	24	25
Nucleotide sequenc	AAH75159	22	755	36.9	24	
Human prostate exp	ABV54779	23	569	36.9	24	
DNA encoding novel	AAS84412	23	452	36.9	24	
Human digestive sy	AAK89195	22	22798	37.2	٠.	21
Human immune/haema	AAK81124	22	22798		•	20
Lung cancer relate	ABL65847	24	2600	•	4	19
Chromatin regulato	AAT43624	17	2600	37.2	4.	18
Arabidopsis thalia	AAC33441	21	1006	•	4	17
Drosophila melanog	ABL14686	23	9477		4	16
Drosophila melanog	ABL14687	23	5668		24.8	15
Drosophila melanog	ABL11216	23	2837	40.6	σ.	14
н	AAA96835	21	243	70.8		13
Nucleotide sequenc	AAA96856	21	600	84.6	55	12
	AAA96854	21	462	84.6		11
Nucleotide sequenc	AAA96853	21	393	84.6		10

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ALIGNMENTS

RESULT 1
ARAS6842
ID ARAS9
XX ARAS9
XX ARAS9
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XX Dire
XX Prom
KW Prom
KW Chin
KW Uran
XX W Plar
XX W Plar
XX W FOO
PD 05-C
XX W 29-A
XX WPI
PR RANC
XX WPI
PT Chin Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; 05-OCT-2000. Synthetic. transgenic plant; ss Directional desoxymucleotide building block S1. AAA96842; AAA96842 standard; DNA; 65 BP Rance I, 29-MAR-1999; 29-MAR-2000; 2000WO-IB00370 WO200058485-A1. 19-FEB-2001 MERISTEM THERAPEUTICS Gruber V, (first entry) 99FR-0003925 Theisen M;

Nucleotide Nucleotide Nucleotide

Chimeric expression promoter for transgenic plant production, comprises

WPI; 2000-647238/62

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RESULT 2
AAA96837
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                            Chimeric sequence
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are
         with
                                                                                               WPI; 2000-647238/62.
                                                                                                                                                                                                                                                                                                                           ·05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96837 standard; DNA; 317
                                                                                                                                            Rance
                                                                                                                                                                                                                                  29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence from with sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             producing transgenic plants.
eric expression promoter for transgenic plant production, comprisence from promoter comprising vascular expression region replaced sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAA 60
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                                                                                                                                                                                      MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression promoter; plant vasomentissue expression promoter; ic plant; chimera; ss.
                                                                                                                                         Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                               Cassava vein mosaic virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 20 A; 16 C; 14 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                               2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter comprising vascular expression region replaced from promoter comprising green tissue expression region
                                                                                                                                                                                                                                  99FR-0003925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                         Theisen M;
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Pred. No. 5.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular expression promoter;
cer; Cassava vein mosaic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter MPr1116
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English

The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from

from

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RESULT 3
AAA96839
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                             Chimeric expression promoter for transgenic plant production, or sequence from promoter comprising vascular expression region rewith sequence from promoter comprising green tissue expression
                                                                                                                                                                                                                                                                                                                                           05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric expression promoter; plant green tissue expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA96839;
                                                                                                        Claim 5;
                                                                                                                                                                                                      WPI; 2000-647238/62
                                                                                                                                                                                                                                 Rance I,
                                                                                                                                                                                                                                                                                      29-MAR-1999;
                                                                                                                                                                                                                                                                                                                 29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                      WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96839 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 317 BP; 107 A; 61 C; 74 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for producing transgenic plants.
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                                                              present sequence represents a chimeric promoter of specification describes chimeric expression promote
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                                                                                                                                                                                                                                                            MERISTEM THERAPEUTICS.
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                                                                                                      Page
                                                                                                                                                                                                                              Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of chimeric expression promoter MPr1146.
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                                                                                                        81; 91pp; English.
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Pred. No. 8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant vascular expression promoter; promoter; Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 T; 0 other;
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Best Local (
              The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commellina yellow mottle virus, and the second plant promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                     Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96838 standard; DNA;
                                                                                                                                                                                                                                                                                       Claim 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic plant; chimera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TAGCT 72
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  producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                     Page 81; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression promoter; plant vascular expression en tissue expression promoter; Cassava vein mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 BP; 122 A; 68 C; 89 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of chimeric expression promoter MPr1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cassava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Commelina yellow mottle virus. Cassava vein mosaic virus.
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transgenic plants.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mosaic virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric expression promoter for transgenic plant production, compris-
sequence from promoter comprising vascular expression region replaced
with sequence from promoter comprising green tissue expression region
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                                                                                                                                                                                                                                                  producing transgenic plants.
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                                               CAGACTAGTATCCGCCGTCATCAATGACATCATCACCAGTACTGAGGAGATGAATAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERISTEM THERAPEUTICS
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                     398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commelina yellow
Cassava vein mosa
                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 398
                                                                                                                                                                                                   A; 80 C;
                                                                                                                      100.0%;
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                                                                                                                                                 89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mottle virus
                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
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                                                                                                                         Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant vasc
                                                                                                                                                                                                     93
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular expression promoter;
ter; Cassava vein mosaic virus
                                                                                                                                                                                                     97 T; 0 other;
                                                                                                                      DB 21; ; 3.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; 1
3.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter MPr1147
                                                                                                                                              Length 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 348
                                                                                                 Indels
                                                                                                 0
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106
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SEEXBXBXBXB
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                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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Best Local :
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a chimeric promoters. These chimeric promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelima yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; chimera; ss.
                                                          Nucleotide sequence of chimeric expression promoter MPr1168
                                                                                           19-FEB-2001
                                                                                                                                                   AAA96858 standard; DNA;
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1999;
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleot1de sequence of chimeric expression promoter MPr1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2001
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                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                 CAGACTAGTATCCGCCGTCATCAATGACATCATCACCAGTACTGAGGAGATGAATAGCT 65
                                                                                                                                                                                                                            CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-647238/62
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                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                472 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Commelina yellow mottle virus.
                                                                                                                                                                                                                                                                                     Conservative 0;
                                                                                         (firet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99FR-0003925
                                                                                                                                                                                                                                                                                                                                               149 A; 92 C; 112 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                        entry)
                                                                                                                                                                                                                                                                                 89.2%; Score 58; DB
100.0%; Pred. No. 3.9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theisen M;
                                                                                                                                                   541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472
                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                    3.9e-12;
hes 0;
                                                                                                                                                                                                                                                                                                                   DB 21;
 pression promoter;
vein mosaic virus;
                                                                                                                                                                                                                                                                                                                Length 472;
                                                                                                                                                                                                                                                                                    0;
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AAA96857
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                            Chimeric
Chimeric
                                                                                                                                chimeric expression promoter; plant vascular expression plant green tissue expression promoter; Cassava vein mos transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric expression promoter for transgenic plant production, c sequence from promoter comprising vascular expression region re with sequence from promoter comprising green tissue expression
                                                                                                                                                                                                       Nucleotide sequence of chimeric expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 541 BP; 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric -
Chimeric -
                                                                WO200058485
                                                                                                                                                                                                                                  19-FEB-2001
                                                                                                                                                                                                                                                                                       AAA96857 standard; DNA; 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic plant; chimera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI-) MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                   8 CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGGATGAATAGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a chimeric promoter of the invention specification describes chimeric expression promoters. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                       CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            υ
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                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 87-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruber V,
                                                                                                                                                                          intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commelina yellow mottle virus.
                                                                                           Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99FR-0003925.
                                                                                                                                                                                                                                                                                                                                                                                                         89.2%; but
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 104 C; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theisen M;
                                                                                                                                                                                                                                                                                       ₽P.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 138 T;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
4e-12;
                                                                                                                                                 Cassava vein mosaic virus;
                                                                                                                                                                                                     promoter MPr1167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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29-MAR-2000; 2000WO-IB00370

05-OCT-2000.

29-MAR-1999;

99FR-0003925.

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RESULT 9
AAA96855
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transcenic regions.
Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                     Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence from with sequence
                                                               WPI; 2000-647238/62
                                                                                                                                                       29-MAR-1999;
                                                                                                                                                                                  29-MAR-2000;
                                                                                                                                                                                                                                                                           Chimeric - Commelia
Chimeric - Cassava
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA96855 standard; DNA; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
                                                                                                                                                                                                                                                WO200058485-A1
                                                                                                                         (MERI-) MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression promoter for transgenic plant production, compris-
from promoter comprising vascular expression region replaced
uence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 87; 91pp; English
                                                                                           Gruber V,
                                                                                                                                                                                                                                                                         Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                    2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic
                                                                                                                                                       99FR-0003925.
                                                                                                                                                                                                                                                                                                                                                                                                   of chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.2%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises
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Matches
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                           The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commellina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are
                                                                                                                                                                                                           Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                        derived from intergenic regions. The chimeric promoters are useful
20
                           11 ACTAGTATCCGCCGTCATCAATGACATCACCAGTACTGAGGAGATGAATAGCT
                                                                                                                                 Local
                                                                                                                                                                                                                                                         producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a chimeric promoter of the invention
ACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Page
                                                                                                                                 Similarity
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91pp; English.
                                                                                                                              100.0%;
                                                                                                                                                       84.6%;
                                                                                                     0;
                                                                                                                              Score :
                                                                                                     Mismatches
                                                                                                                              . 55;
                                                                                                                                                       BB
                                                                                                                                                       21;
                                                                                                                                                       Length 392;
                                                                                                     Indels
                                                                                                     0
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AAA96853
                                                                                                                                                                                                                                                                                                                      RESULT 10
                                 Chimeric -
                                                                                                                        chimeric expression promoter;
                                                                                                                                                                                                                 19-FEB-2001
                                                                                                                                                                                                                                                  AAA96853;
                                                                                                                                                                                                                                                                                     AAA96853 standard;
WO200058485-A1
                                                                                                                                          Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                               Nucleotide
                                                                                                       green
                                 Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                     plant;
                                                                                                                                                                          sequence of chimeric expression promoter MPr1162
                                                                                                       tissue expression
                                                                                                                                                                                                               (first entry)
                                                                                       chimera;
                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                     393
                                                                                        88
                                                                                                                                                                                                                                                                                     ΒP
                                                                                                   plant vascular expression promoter; promoter; Cassava vein mosaic virus
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29-MAR-1999;

99FR-0003925

MERISTEM THERAPEUTICS.

29-MAR-2000; 2000WO-IB00370

05-OCT-2000.

Rance

Gruber V,

Theisen M;

2000-647238/62

The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from

from

Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region

Claim

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Page 85;

91pp; English

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RESULT 11
AAA96854
    Best Loc
Matches
                                               Query Match
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Best Local
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                                                                                                                                                       The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from commeltina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; chimera; 68.
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 86; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-647238/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Commelir
Chimeric - Cassava
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96854 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 393 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI-) MERISTEM THERAPEUTICS
                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT 74
       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                              462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Commelina yellow mottle virus.
       Conservative
                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-IB00370
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                                                                                                                                      transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99FR-0003925.
                                                                                            148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 A; 75 C; 93 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of chimeric expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
84.6%; Score 55; DB
100.0%; Pred. No. 5.:
Live 0; Mismatches
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100.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theisen M;
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                                                                                            87 C; 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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                                                                                         ဝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 55;
                                                                                            116 T;
                     DB 21; 1
5.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
5e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Length 393,
                                                                                            0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                            Length 462;
  Indels
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0;
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AAA96835;

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RESULT 13
AAA96835
ID AAA96
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AAA96856
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                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                      The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic transgenic plant; chimera; ss.
                                        AAA96835 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
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                                                                                                                                                                                                                                            for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of chimeric expression promoter MPr1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-2001
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                                                                                                                                                                             Local
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••
                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                    600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Commelina yellow mottle virus.
                                                                                                                                                                                                                                                                                                                                                                    sequence represents a chimeric promoter of the invention
                                                                                                                                                                Conservative
                                                                                                                                                                                                                    BP; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                            86-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99FR-0003925
                                        DNA;
                                                                                                                                                         84.6%; but
100.0%; Pr
                                                                                                                                                                                                                    A; 111 C; 147
                                                                                                                                                                                                                                                                                                                                                                                                          91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Theisen M;
                                        243
                                                                                                                                                               Score 55; DB:
; Pred. No. 5.60
0; Mismatches
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                                                                                                                                                                                                                   G; 154 T;
                                                                                                                                                                           .6e-11;
                                                                                                                                                                                        21;
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                                                                                                                                                                                                                    other;
                                                                                                                                                                                          Length 600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter;
                                                                                                                                                               <u>,</u>
                                                                                                            74
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19-FEB-2001

(first entry)

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ABL11216
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   construct chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region i replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassan control of the control of the cassan control of the control of the cassan 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mottle virus, and t
vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus;
                       WO200171042-A2
                                                                      Drosophila melanogaster
                                                                                                                    pharmaceutical; gene;
                                                                                                                                              Drosophila;
                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 28130
                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                              ABL11216 standard; cDNA; 2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 243 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter in vascular and reproductive tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a promoter fragment from the intergenic region of Commelina yellow mottle virus. The promoter is a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 79; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-647238/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI-) MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gruber V,
                                                                                                                                            developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intergenic region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 53 C; 45 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The promoter is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                              insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises
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RESULT 15
ABL14687/c
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Best Local S
Matches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2837 BP;
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11-JUL-2000; 2000US-0614150.
         WPI; 2001-656860/75
                                Venter JC,
                                                                             23-MAR-2000;
11-JUL-2000;
                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                            pharmaceutical;
                                                                                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 38543
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                              Adams M,
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                                                                             2000US-191637P
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Search completed: May 11, 2003, 03:04:00 Job time : 128.416 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2: /cgn2_6/ptodata/1,

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Sequence 82, Appl	Sequence 162, App	Sequence 3, Appl	Sequence 72, App.	Sequence 65, App.	Sequence 373, App	Sequence 6, Appli	Sequence 4, Appli	Sequence 3, Appli	•	Sequence 9, Appl	Sequence 9, Appl:	Sequence 9, Appl	Sequence 9, Appl:	Sequence 7, Appl:	Sequence 7, Appli	Sequence 7, Appl:	Sequence 7, Appli

ALIGNMENTS

RESULT 1 US-09-183-861-77/c

Sequence 77, Patent No. 6

7, Application US/09183861 6365165

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

Campos-Neto, Webb, John R.

Antonio

NUMBER OF SEQUENCES:

T: Dillon, Davin C. T: Skeiky, Yasir A.W. INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND

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; TOPOLOGY: linear US-09-183-861-77
Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.4200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STATE: Washingt
COUNTRY: USA
                                                                                                         LENGTH: 1086 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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         Conservative
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                       34.2%;
                     Score 22.2;
Pred. No. 2
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         Mismatches
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Patrent No. 6375955
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
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INFORMATION FOR SEQ ID NO: 77:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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   Hodgson, John E.
                  Pratt, Julie M.
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Query Match
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RESULT 4
US-08-785-310A-3
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Sequence 3, App....
No. 5840532
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GM10107
CURRENT APPLICATION NUMBER: US/09/147,926
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/061,077
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                TELEFAX: (415) 343-434
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus aureus FEATURE: NAME/KEY: CDS LOCATION: (1)...(1176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 1ECHNOLOGY LAW GROUP
CORRESPONDENCE SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Neuronal PAS Domain Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Russell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 ACGCTGTGACGAAGTAGCTACCTGCAACAATGGCATCATTGCCCCATATGTGGTGATGAA 597
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/C
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
                                                                    TOPOLOGY: 1i
                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALIFORNIA
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Deresiewicz, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beattie, David T.
Lowe, Adrian M.
                                                                                                                     4010 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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                                                                      linear
                                                    CDNA
                                                                                     double
                                                                                                                                                                          343-4342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  David W
33.8%;
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                                                                                                                                                                                                                                                                                                                                    US/08/785,310A
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 Score 22;
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Pred. No. 2
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DB 2;
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Length 4010;
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SEQ ID NO 143
LENGTH: 1515
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Patent No. 5972899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 638037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            SOPTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 ATGCTGGAGAATTCTATACGCCATCATCAATTGTAAAATTA 537
                                                                                                          NAME: Livnat, Shmuel REGISTRATION NUMBER: 33,949
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                                   TELEFAX:
                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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               (202) 887-0764
0-4030 MRSNFOERSWSH
                                                                                                                                                                                                                                                                                                                                                             USA
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Pred. No. 3
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                                                                                                                                                                                                                                             Version #1.30
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PCT-US96-03916-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                          TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: White, John P.
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 24-SEP-1993
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                          FEATURE:
                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                              HYPOTHETICAL:
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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NAME/KEY:
                                       NAME/KEY:
LOCATION:
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LOCATION: 543..23:
OTHER INFORMATION:
                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                  STRANDEDNESS:
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                                                                                                        POPOLOGY:
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                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                10036
                                                                                                                                nucleic acid
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Y: U.S.A.
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1185 Avenue of the Americas
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543..2324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild, Martha A.
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2575..4107
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                                                                                          (genomic)
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Pred. No. 45;
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Db 11397 TTTCCTCCGTCGTAAATTAAATCATGAAAGCAATAGTTAGGCGAAGAGC 11349
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Best Local Similarity
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
                                                                                       TELEPHONE: (212) 278-041
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 NAME: White, John P. 28,678
REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                             APPLICATION NUMBER: US 08/126,597 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
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NAME/KEY:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark E
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NAME/KEY:
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ITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
ITLE OF INVENTION: AND USES THEREOF
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LOCATION:
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                                          STRANDEDNESS:
                               TOPOLOGY:
                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                         nucleic acid
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1185 Avenue of the Americas
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11159..12658
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9874..10962
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4609..5487
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4113..4445
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                               linear
              DNA (genomic)
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Pred. No. 56;
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US-08-484-105-1/c
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                                                                            Query Match
                                                   Matches
14030 TTTCCTCCGTCGTAAATTAAATCATGAAAGCAATAGTTAGGCGAAGAGC 13982
                                                                                                                                                                                                                                                                                                                 FEATURE:
                         16 TATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGC 64
                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 16129..17013
OTHER INFORMATION:
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LOCATION: 13792..15291
OTHER INFORMATION:
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LOCATION:
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LOCATION:
                                                  Local Similarity 65.1
les 32; Conservative
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LOCATION: 15298..
OTHER INFORMATION:
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LOCATION:
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LOCATION:
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LOCATION:
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OTHER INFORMATION:
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5210..7081
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8333..11290
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697..1533
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11098..12402
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3694..5124
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                                                              33.5%;
                                                Score 21.8; D
Pred. No. 61;
0; Mismatches
                                                                          DB 5;
                                                   17;
                                                                          Length 18912;
                                                   Indels
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Sequence 1, Application US/08484105 Patent No. 5589341 GENERAL INFORMATION:

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APPLICANT: APPLICANT:

BELL, Stephen P KOBAYASHI, Ryuji RINE, Jasper

STILLMAN, Bruce

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RESULT 10
US-08-484-106-1/c
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Best Local Similarity 68.2
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                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                        3721 GCCAGCAACATCGACATCATAACAAAAGTCAGGATAGAAAGAGC 3678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEFX: 910 277299
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NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-5903:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                    APPLICANT:
                                                                                                                          TITLE OF
                                                                                                                                                       APPLICANT
                                                                                                                                                                                                                   APPLICANT
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FILING DATE:
CLASSWITCATION: 435
                           CITY: San
STATE: Cal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        STREET:
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                OUNTRY:
                                                                         ADDRESSEE:
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94111-4187
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                                                                                                                        T: GAVIN, Kimberly 
INVENTION: ORIGIN
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                                                        4 Embarcadero Center,
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McNALLY, Francis J
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                                                                                                                                                                                                                                                          BELL, Stephen P
                                                                                                                                                               LAURENSON, Patricia
HERSKOWITZ, Ira
                                                                                                                                                                                                                                                                            STILLMAN, Bruce
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                                           Francisco
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                                                                       FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
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                                                                                                                      ORIGIN OF REPLICATION COMPLEX GENES
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Pred. No. 52;
0; Mismatches
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                                                            Suite 3400
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RESULT 12
US-09-419-291A-3/c
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; ORGANISM: Homo sapiens
US-09-112-450-3
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                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 8561
GENERAL INFORMATION:
              Sequence 3, Application US/09419291A Patent No. 6416989
                                                                                                                                                                                          Best Local Similarity Matches 24; Conserv
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Best Local Similarity
                                                                                                                                                                                                                              Query Match
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APPLICANT: Choi, Gil
APPLICANT: Calderone, Richard A.
TITLE OF INVENTION: Histidine Kinase Two-component in Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/112,450 CURRENT FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/074,308
EARLIER FILING DATE: 1998-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/052,273
EARLIER FILING DATE: 1997-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PF393
                                                                                                                       5413 TAATCAATGACAACATGACAATACTGAG 5386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/484,106 FILING DATE:
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DEDNESS: double
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85.7%;
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Pred. No. 6
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Pred. No. 52
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; TYPE: DNA
; ORGANISM: Candida albicans
US-09-419-291A-3
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Best Local Similarity
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR PILING DATE: 1999-05-07
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SOFTWARE: Patent.pm
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CURRENT APPLICATION NUMBER: US/09/419,291A
CURRENT FILING DATE: 1999-10-15
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LOCATION? 501
OTHER INFORMATION: 12-406-52 : polymorphic base C or
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                  OTHER INFORMATION: downstream amplification primer, complement
                                               NAME/KEY: primer_bind
LOCATION: 881..899
                                                                                                                               NAME/KEY: misc_binding
LOCATION: 502.521
OTHER INFORMATION: 12-406-52.mis2, potential complement
NAME/KEY: primer_bind
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LOCATION: 481.500
DTHER INFORMATION: 12-406-52.misl, potential
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RGANISM: Homo Sapiens
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UMBER: US 60/119,917
1999-02-12
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1999-05-07
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Pred. No. 60;
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                  Query Match
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
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LOCATION: 4,53,104,243,324,369
OTHER INFORMATION: n=a, g, c o
                                                                               NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 12,717,742,755,758,1000..1001
                                                                                                                                                                                                                                                                              NAME/KBY: misc_binding
LOCATION: 502..521
COTHER INFORMATION: 12-406-409.mis2, potential complement
NAME/KBY: primer_bind
                                                                                                                                           OTHER INFORMATION: 12-406-409 potential probe
                                                                                                                                                             NAME/KEY: misc_binding LOCATION: 489..513
                                                                                                                                                                                             OTHER INFORMATION: upstream amplification primer NAME/KEY: primer_bind LOCATION: 524..542.
OTHER INFORMATION: downstream amplification primer,
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                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US (FILING DATE: 1999-03-23 APPLICATION NUMBER: US (FILING DATE: 1999-02-12
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Score 21.2; D
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24 GTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT 65

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RESULT 15
US-09-362-831-10/c
; Sequence 10, Application US/09362831
; Patent No. 6306400
; GENERAL INFORMATION: AVIAN RECOMBINANT LIVE VACCINE USING, AS VECTOR, THE TITLE OF INVENTION: AVIAN RECOMBINANT LIVE VACCINE USING, AS VECTOR, THE CURRENT PAPLICATION NUMBER: US/09/362,831
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Result
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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AZ952780	AA390522	264	BQ378960	AW971534	AA814930	AA235966	BE748221	AZ217624	AZ218097	CNS07CX4	BQ097606	BM052014	AG064170	AI344331	AI344310	BQ898008 .	BQ884980	BG293515	BI739607	BQ745618 .	BG969043	AI747024	BF348858	BB638327	BB655827	BB651874	BB618417	BB659983	BB621994	BI715981	BI713238	BQ562476	BE531686	BM942017		NS01SA	BE975786	414	
AZ952780 2M0217C18	D08708.		BQ378960 RC3-UT006	AW971534 EST383623	AA814930 oc07c03.s	AA235966 zs05f02.s	BE748221 601571441	AZ217624 Sheared D	AZ218097 Sheared D	AL439742 T7 end of	BQ097606 ph05a07.y	BM052014 Tc_ad2_02	AG064170 Pan trogl	AI344331 tc03f12.x	AI344310 tc03d11.x	BQ898008 AGENCOURT	BQ884980 AGENCOURT	BG293515 602390444	BI739607 603361862	BQ745618 UI-M-EW0-	BG969043 602834988	AI747024 ull2e04.y	BF348858 RC1-DT002	BB638327 BB638327	·BB655827 BB655827	BB651874 BB651874	BB618417 BB618417	BB659983 BB659983	BB621994 BB621994	17159	BI713238 ic85h09.y	5624	16	420	66720	L164981 Tetr	975786 bs45c	034140 Homo	

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL COMMENT SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 BF168473/c LOCUS FEATURES DEFINITION source Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9267 row: a column: 17 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 614)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. 614 bp mRNA linear EST 30-OCT-2000 601776065F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017688 5', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus BF168473 BF168473.1 GI:11048825 house mouse. quality sequence stop: 614.
Location/Qualifiers

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563 665 814 785 769

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ACCESSION
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                                                                                                                                                                                                                                                           This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PBST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microganisms that inhabit the Gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neontera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Class: BAC ends.
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1 (bases 1 to 563)

Shetty, J., Malek, J., Koo, H.,
Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH372871 563 bp DNA linear GSS 10-DEC-2001
AG-ND-106G18.TR ND-TAM Anopheles gambiae genomic clone AG-ND-106G18
                                                                                                                                                                                                                                            partial digest
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Other_GSSs: AG-ND-106G18.TF
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      157
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8 97 c 154 g 164 t 1 others
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/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_nost="DH108"
/clone="AG-ND-106G18"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
107 c 83 g 216 t
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/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4017688"
                                                                                         db_xref="taxon:7165"
                                                                                                                                    organism="Anopheles
                                                                                                                                                                             Location/Qualifiers
                                                                                                                strain="PEST"
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Pred. No. 18;
0; Mismatches
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                                                                                                                                  gambiae"
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                                      341 ATTTTGCAGCAGAGTAAAGACCTTACGGAAGGACAATATCAGATTACAGAGGAAATGAAT 282
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   62 A 62
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                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 03643
Email: bjloftuserigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center library was constructed at Texas A&M University BAC Center
                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Normara: Endonteryqota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                      partial digest.
Seq primer: M13 Rev
Class: BAC ends.
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AG-ND-106B1.TR ND-TAM Anopheles
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                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         University, College Station,
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/Clone="hG-ND-106B1"
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/note="Vector: pECBAC1; Site_1: HindIII"
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                                                                                                                                                                                                                                                                                                 organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                     strain="PEST"
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BAC-end
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                                                                                                         Score 27.4; D
Pred. No. 41;
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Pred. No. 3
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: biloftuserigr.org
Email: biloftuserigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA, All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                         785 bp
GM830013A20F02 Gm-r1083 Glycine
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Seg primer: M13 For
Class: BAC ends.
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae
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AG-ND-172C15.TF ND-TAM Anopheles gambiae genomic clone AG-ND-172C15
                                                                       EST
                                                                                          BI971380.1 GI:16345785
                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="AG-ND-172C15"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
141 c 132 g 304 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="PEST"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27.4; D
Pred. No. 45;
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lone Gm-r1083-4852
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Best Local :
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269 TGCTTCAGCTTCATCTTCACCGCCATTGATGACATCATTAAGGTACTCCTGAGCTTCAT 327
                                                       3 TGCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAAT 61
                                                                                                                         39;
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Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other ESTs: BE022118 corresponding to Gm-c1028-9003 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. anv A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Illinois
Edwin R. Madigan Building,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: 5'-TTTTTTTTTTTTTTTTT (A/C/G)-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio
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                                                                                                                                                                                                                                                                               220
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                            /clone="Gm-1083-4852"
/clone="Gm-1083-4852"
/note="The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-c1009 (from mature roots of 2 month old greenbouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-c1013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-c1028 (from 'Supernod' plants whose seedlings were innoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor library see sused to select singletons, or a representative of each contig, which were reracked to form library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfsoy/.

Reracking was performed by Incyte Genomics, St. Louis, http://www.incyte.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.lie.uic.edu/biotech/keck.html.

Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

247 f 7 others
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db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                               390 CATTACACAGAACAGTATCAGCACACAGCAGGCACTTGATAAAAGTATTGAATAAATGAA 331
                                                                                                                                                                                                                                                                                                                                                                                       61 TA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CATGCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAA 60
                                                                                                                                                                                                                                                                                                                                              TA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                             IMAGE: 4610636,
BC034140
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                   Strausberg, R
                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                               Homo sapiens
                                                                                                                    human.
                                                                                                                                                            BC034140.1
                                                                                                                                                                                                                      BC034140
Homo sapiens, Similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLCM1356 row: c column: 21
High quality sequence stop: 741.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Income Library Arrayed by: The I.M.A.G.E. Consortium
                                      (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4610636"
/clone lib="NIH MGC 75"
/lab host="DYS"
/lab host="PH10B (TI phage-resistant)"
/lab host="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgtctggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGATGGCC3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGATGGCGG3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGATGGCGGCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

15 a 122 c 178 g 253 t 1 others
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                                    to 968)
                                                                                                                                                            GI:21707881
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: f Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7662105
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                Laboratory of Cellular and Developmental Biology NIDDK, National Institutes of Health 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethe Fax: (301) 496 5239
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE975786 543 bp mRNA linear EST 04-OCT-200 bs45c02.x1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs45c02 3', mRNA sequence.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                 BE975786.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster cDNA clone
BE975786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328
Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed
                                                                                                                                                          Contact: Brian Oliver
                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                       Andrews, J., Bouffard, G. and Oliver, B. Drosophila melanogaster testis expressed
                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                      fruit fly.
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/db_xref="taxon:9606"
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clone lib="NIH MGC 75"
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Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ALI64981
ALI64981.1 GI:7802719
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                              Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fishn Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis Tetracdon nigroviridis DNA sequence
                                                                                                                                                     Roest-Crollius, H., Jaillo Bouneau; L., Billault, A., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).

Plate: 45 row: c column: 02
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169B05 of library G from Tetraodon
                                   Genoscope.
                                                                                Unpublished
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                                                                                                                                                                                                                                           Unpublished
                                                                                                          freshwater pufferfish
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                                                           (bases 1 to 772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."
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/strain="y[*] w[67c1]/Y"
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lt,A., Quețier,F., Saurin,W.,
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Pred. No. 83;
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n,W., Bernot,
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A. and
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                                                                                                                                                                                                                                                                                                                                                                     Bmail: mBST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF466720 103 bp mRNA UI-M-CG0p-bqx-f-04-0-UI.81 NIH BMAP Ret4 S UI-M-CG0p-bqx-f-04-0-UI 3', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chin,
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Fax: 301 443 9890
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1 (bases 1 to 103)
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                  /clone="UI-M-CGOp-bqx-f-04-0-UI"
/clone lib="WIH BWAP Ret4 S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH BWAP Ret4 S2 library is a subtracted library,
ultimateIy derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
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/db_xref="taxon:99883"
/clone="169B05"
/clone_11b="G"
/clone_1ib="G"
/note="Genoscope sequence ID : COM-
PUC-Ori"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                 organism="Mus musculus"
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1. Room 7N-7190, MSC 9643, Bethesda,
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Pred. No. 1.1e+02;
1; Mismatches 19;
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site at brainest.eng.uiowa.edu.
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BMAP_Ret4_S2 Mus musculus cDNA clone
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Best Local S
Matches 35
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UI-M-CGOp-bqx-f-04-0-UI.rl NIH BMAP Ret4 S
UI-M-CGOp-bqx-f-04-0-UI 5', mRNA sequence.
RM942017
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Eukaryota; Metazoa;
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Seg primer: M13 REVERSE.
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20892-9643, USA
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                                                                                                        /Strain="C57BL/GJ"
/db xref="taxon:10090"
/clone="UI-M-CG0p-bqx-f-04-0-UI"
/clone=lib="NIH BMAP Ret4 S2"
/lab höst="DH10B (Life Technologies)"
/lab höst="DH10B (Life Technologies)"
/lab höst="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH BMAP Ret4 S2 library is a subtracted library, ultImmtely derived from mouse retina tissue library, various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Pu, Yale University School of Medicine"
35 a 39 c 29 g 32 t
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                              Score 26; DB
Pred. No. 61;
0; Mismatches
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Sciurognathi; Muridae;
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ulus cDNA clone
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H4076B12 5', mRNA sequence.
BQ562476
BQ562476.1 GI:21463362
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 545)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T., Kargul, G.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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Mammalla; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 482)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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601230802F1 NCI_CGAP_Mam6
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                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAM8769 row: d column: High quality sequence stop: 482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE531686.1
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                                                                                                                                                                                                                                                                                                                                                                                           40.0%;
ilarity 70.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clome="IMAGE:3594577"
/clome lib="NCI CGAP Mam6"
/exx="female, vIrgin"
/sex="tissue_type="infiltrating di
/dev stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" a 113 c 97 g 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 26;
Pred. No.
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s musculus
                                                                                                                                                                                                           Clone Set Mus musculus cDNA clone
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. 1.1e+02;
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A clone
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IMAGE:3594577 5',
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TITLE
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AUTHORS
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BI713238/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGAGAATAGGAAACGCCGGCATGGATGAGCTCACCAGACTAATGTGG 111
                                                                                            Other ESTs: ic85h09.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cam
                                                                                                                                                                                                               Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4076 row: B column: 12
Seq_primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Insti
333 Cassell Drive, Suite 3000, Baltimore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI713238
549 bp mRNA linear EST 12-MAR-2002 ic85h09.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus CDNA clone IMAGE:5660776 5' similar to TR:Q9VZ81 Q9VZ81
                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI713238
BI713238.1 GI:15688933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus cDNA clone CG13708 PROTEIN. ;,
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
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                                         617-495-1812
617-495-8557
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113 c 104 g 152 t
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ell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="H4076B12"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="niaEST:H4076B12-5"
/db_xref="taxon:10090"
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Rodentia;
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Pred. No. 1.1e+02;
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Divinity Ave, Cambridge,
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AUTHORS
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BI715981/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                      KEYWORDS
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JOURNAL
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256 GCTGGAGAATAGGAAACGCCGGCATGGATGAGCTCACCAGACTAATGTGG
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                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 566)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelll, J., Gradwohl, G., Clitton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
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566 bp mRNA linear EST 12-MAR-2002 ic64b03 y2 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5658197 5' similar to TR:Q9VZ81 Q9VZ81 CG13708 PROTEIN. ;, mRNA sequence.
Contact: Douglas Melton, Klaus H. Kaestner, & Hiros
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                        Endocrine Pancreas Consortium 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University Genome Sequencing Center For obtaining a clone please contact: Juliana Brown (brown@fas harvard.edu)
MGI:1947102 This sequence now available from the IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI715981.1 GI:15691676
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                                                                                                                                                      Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Wector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five libraries representing EIO.5/12.5 pancreatic bud, E16.5 pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares normalized by method #100 plasmid DNA was mingle-stranded mixed library plasmid DNA was single-stranded mixed library plasmid DNA was mingle-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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adult, mixed"
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Search completed: May 11, 2003, 04:54:08 Job time : 1049.89 secs
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Matches 35; Conservative
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MGI:1944523 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
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Fax: 617-495-8557
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| db_xref="taxon:10090"
| clone="IMAGE:5658197"
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Sequence 6211, Ap	Sequence 1593, Ap	Sequence 21997, A	Sequence 59, Appl	Sequence 1, Appli	Seguence 3, Appli	-	Sequence 15, Appl	-	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 2430, Ap	Sequence 1, Appli	Sequence 5, Appli	Sequence 25, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 77, Appl	Sequence 77, Appl	Sequence 1, Appli	Sequence 2262, Ap	Sequence 521, App	Sequence 1705, Ap

ALIGNMENTS

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PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR PELICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 65
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Directional desoxynucleotide builty of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
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LOCATION: (1)..(371)
OTHER INFORMATION:
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; Sequence 5? Application US/09963803
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; GENERAL INFORMATION:
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; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
                            Query Match
Best Local Similarity
Matches 65; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: FR 99/0370
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NUMBER OF SEQ ID NOS: 39
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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT 1800/00370
PRIOR FILING DATE: NUMBER: PCT 1800/00370
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                            OTHER INFORMATION: promoter MPr1146
                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    FEATURE:
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OTHER INFORMATION: Promoter MPr1116
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ITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
ITLE OF INVENTION: Virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EATURE
                                                                                                                                                                                                                                                                                                              ENGTH: 371
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QANISM: Artificial Sequence
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1 CATGCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAA 60
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                                    100.0%;
ilarity 100.0%;
Conservative 0
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                                    Score 65; DB 9; Pred. No. 1.1e-15; Mismatches 0;
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Pred. No. 1e-15;
Nismatches 0; Indels
                                                                             Length 371;
                                      Indels
                                    0,:
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US-09-963-803-4
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                                                                                                                                                                                     SEQ ID NO 6
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Publication No. US20030028922A1
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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CURRENT FILING DATE: 2001-09-26
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 184332042
                                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
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                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION
                       NAME/KEY: promoter
LOCATION: (1)..(39
                                                                                 OTHER INFORMATION: promoter MPr1147
                                                                                                                                               TYPE: DNA
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                                                                  EATURE:
                                                                                                                                                                    ENGTH:
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100.0%; Pr
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Publication No. US20030028922A1
GENERAL INFORMATION:
                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 541
                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US20
GENERAL INFORMATION:
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SEQ ID NO 25
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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PR 99/03925
PRIOR FILING DATE: 1999-03-29
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus FILE REFERENCE: 184332042
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                          ORGANISM: Artificial Sequence
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                OTHER INFORMATION: promoter MPr1168
                                       FEATURE:
BATURE:
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100.0%; Pred. No. 5.9e-13;
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100.0%; Pred. No. 6.2e-13;
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US-09-963-803-21

Sequence 21, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapuetics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus

SEQ ID NO 21

TYPE: DNA

392

ORGANISM: Artificial Sequence

NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn ve

version 3.1

PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT 1800/00370
PRIOR FILING DATE: 2000-10-05

CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26

FILE REFERENCE: 184332042

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Publication No. US20030028922A1
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                                                                               Matches
                                                                                                Best Local Similarity
                                                                                                                  Query Match
                                                                                                                                                                             FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(604)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR PPLICATION NUMBER: PR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                    LENGTH: 60
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49 CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAATAGCT 106
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                                      8 CAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGGAGATGAATAGCT 65
                                                                               58; Conservative
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                                                                                                  100.0%;
                                                                                                                    89.2%;
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                                                                                                  Score 58; DB 9;
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                                                                               Mismatches
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RESULT 11
US-09-963-803-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-963-803-19
                                                                                                                                                                                                                                                                      Sequence 20, Application US/09963803 Publication No. US20030028922A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Local Similarity
                                 APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: F99/03925
PRIOR APPLICATION NUMBER: F03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR PILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PT 1800/00370
PRIOR APPLICATION NUMBER: DCT 1800/00370
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: promoter LOCATION: (1)..(393) OTHER INFORMATION:
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OTHER INFORMATION: promoter MPr1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         watch 84.6%; Score 55; DB 9; La Local Similarity 100.0%; Pred. No. 8.7e-12; es 55; Conservative 0; Mismatches 0;
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  PatentIn version 3.1
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100.0%; Pred. No.
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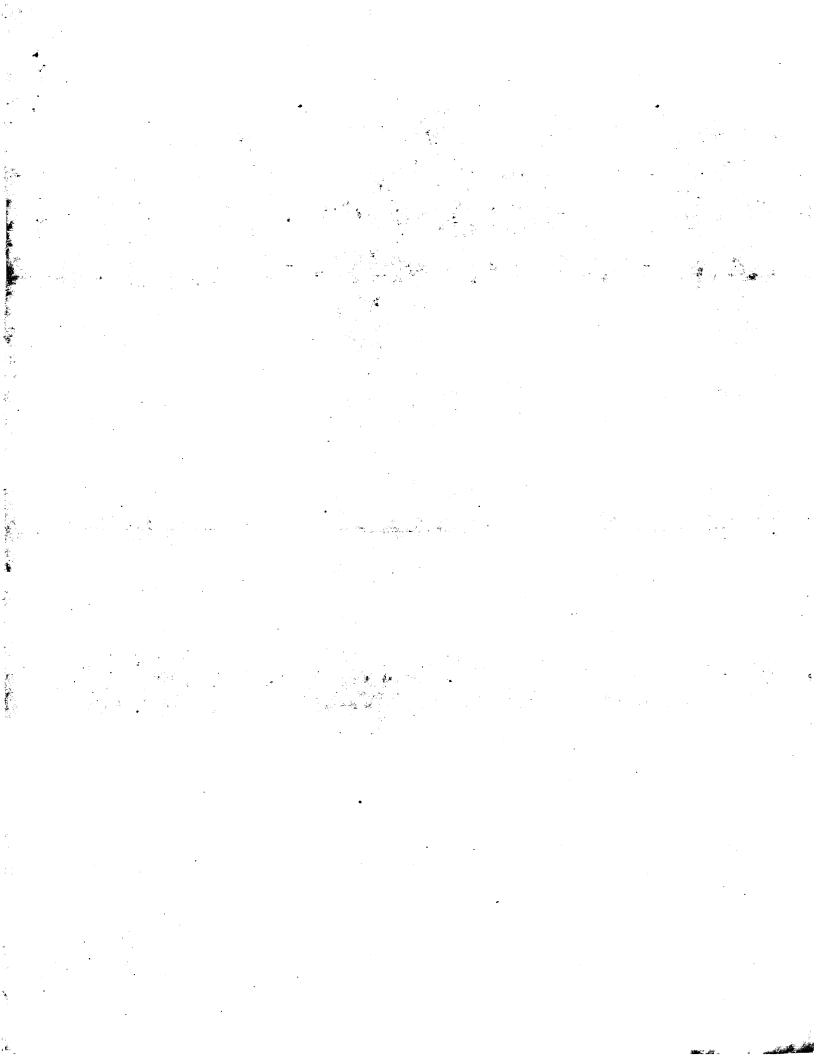
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RESULT 12
US-09-963-803-22
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GENERAL INFORMATION:
APPLICANT: Meristem Therapuetics
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from ITITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR PILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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Publication No. US20030028922A1
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LENGTH: 60
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Best Local
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 1000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
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NAME/KEY: promoter
LOCATION: (1)..(462)
OTHER INFORMATION:
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OTHER INFORMATION: promoter MPrll65
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OTHER INFORMATION: promoter MPr1163
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Pred. No.
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. 9.9e-12;
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; ORGANISM: Homo sapiens
US-09-954-456-1157
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SEQ ID NO 1157
LENGTH: 2600
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Best Local S
                                                                                                                                  Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
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SOPTWARE: PatentIn version 3.1
EQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/235,720 PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-20
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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CURRENT FILING DATE: 2001-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRATURE: OTHER INFORMATION: 243 bp Fragment from the intergenic region of commelina yellow moother Information: ttle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                      676 CTTTCTTCAGGATCGTCTCCATCATCATCATCATCATCATCATTATATTGACCAAGGGCA 617
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108 46; Conservative
  61 T
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                                                              1 CATGCTGCAGACTAGTATCCGCCGTCATCAATGACATCATCACAGTACTGAGGAGATGAA 60
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                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-09-27
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APPLICATION NUMBER: US/60/235,637
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  61
                                                                                                                  Conservative
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62.3%;
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Pred. No.
                                                                                                                                  Score 24.2;
Pred. No. 15;
                                                                                                                Mismatches
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                                                                                                                                                              SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 273
TYPE: DNA
ORGANISM: Homo mapiens
                                                                                                                                                                                                                                                                                                                                                           Sequence 232, Application U
Publication No. US200300082
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
                                                                            Best Local Similarity 86. Matches 26; Conservative
                                                                                                             Query Match
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 1739
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.493C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 T 616
138 CATCGAGGACATCATCACAGTGCTGAAGAG 167
                                         26 CATCAATGACATCACAGTACTGAGGAG 55
                                                                                                                                                                                                                                                                                                                                                                                               Application US/10015219
5. US20030008299A1
                                                                                            36.3%;
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                                                                                            Score 23.6;
Pred. No. 12;
                                                                            Mismatches
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                                                                                                             Length 273;
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                                                                              Gaps
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Search completed: May 11, 2003, 06:11:38 Job time : 67.3484 secs

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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                            score greater than and is derived by a
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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    AAA96844
AAV14022
AAA96837
AAA96839
AAV14019
AAA96855
AAA96853
AAV14021
AAV14026
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/geneseqn-embl/NA1982.DAT:*
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Directional desoxy
CsVMV promoter pC.
Nucleotide sequenc
Nucleotide sequenc
CsVMV promoter CVP
Nucleotide sequenc
Nucleotide sequenc
CsVMV promoter pB.
CsVMV promoter pde
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cDNA encoding nove	AAS40897	22	939	41.9	26	45	
Human cDNA SEQ ID	ABA06449	22	939	41.9	26	44	
Human cDNA clone r	AAK93287	22	833	41.9	26	43	
L1 f	AAI64659	22	1668	42.3	26.2	42	
	AAK91933	22	735	42.9	26.6	41	
	AAV14030	19	491	63.2	39.2	40	
CsVMV promoter pde	AAV14033	19	441	•	40.6	39	
Nucleotide sequenc	AAA96857	21	604	80.6	50	38	
Nucleotide sequenc	AAA96858	21	541	80.6	50	37	
	AAA96859	21	472	80.6	50	36	
	AAA96840	21	398	•	50	35	
	AAA96838	21	348	80.6	50	3 4	
segn	AAA96841	21	301	80.6	50	ω ω	
oter	AAV14023	19	261	90.0	55.8	32	
CsVMV promoter pde	AAV14027	19	482	90.6	56.2	31	
Binary vector DNA	AAD36732	24	12241	100.0	62		a
Tomato anthocyanin	ABQ73049	24	12241	100.0	62		n
pAGI4002 binary ve	AAD24139	24	8340	100.0	62		O
Binary vector pAGI	ABA04755	24	8340	100.0	62		(3
4-Hydroxyphenylpyr	ABL58082	24	8187		62	26	
4-Hydroxyphenylpyr	ABL57989	24	4677	•	62	25	
4-Hydroxyphenylpyr	ABL57988	24	1839	•	62	24	
Nucleotide sequenc	AAF55510	22	931	•	62		O
Nucleotide sequenc	AAF55510	22	931	100.0	62	22	
	AAF55509	22	931	•	62	21	
	AAF55508	22	857	•	62	20	
	AAF55506	22	853	•	62	19	
	AAA96856	21	600		62	18	
Nucleotide sequenc	AAF55507	22	593	•	62	17	
Cassava Vein Mosai	AAD11575	22	532	100.0	62	16	
CsVMV promoter pA.	AAV14018	19	526	•	62	15	
CsVMV promoter CVP	AAV14020	19	524	100.0	62	14	
Nucleotide sequenc	AAF55505	22	515	8	62	13	
Promoter from inte	AAA96836	21	515	80.	62		
CsVMV promoter. C	AAV14053	19	476	Ō	62	11	
Nucleotide sequenc	AAA96854	21	462	100.0	. 62	10	

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ALIGNMENTS

RESULT 1
AAA96844
ID AAA96
AX AAA96
AX AAA9
AX Dire
XX Pron
KW Pron
KW Chim
KW plan
KW plan
KW Wola
XX Wola
PN WO20
XX O5-C
XX O5-C
XX O5-C
XX WFF 29-M
PF 29-AAA96844 standard; DNA; 62 ₽₽

AAA96844;

19-FEB-2001 (first entry)

Directional desoxynucleotide building block S3

Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic transgenic plant; ss. plant vascular expression promoter;
promoter; Cassava vein mosaic virus;

Synthetic

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370

29-MAR-1999; 99FR-0003925.

MERISTEM THERAPEUTICS.

Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62

Chimeric expression promoter for transgenic plant production, comprises

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RESULT 2
AAV14022
ID AAV1
AC AAV1
AC AAV1
AC AAV1
AC AAV1
AC CASE
KW CASE
PN WO97
AXX (SCI
XXX AV1
AXX CASE
PT DNA
PT DN
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Best Local :
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             This sequence represents a cassava vein mosaic virus promoter, and is a nucleic acid molecule of the invention. The promoter is capabinitiating transcription of an operably linked heterologous nucleis sequence in a plant cell. The CSVMV promoters are active in both mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence from with sequence
                                                                                                                                                                                                                                                             Cassava vein mosaic virus promoter - used to express heterologous DNA sequences for producing transgenic plants having altered
                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-063157/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cassava vein mosaic virus;
tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CsVMV promoter
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                                                                                                                                                                         77-78;
                                                                                                                                                                                                                                                                                                                                                                                                                      Kochko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0020129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSVMV; promoter; cultivated crop; control; transgenic plant; ss.
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Pred. No. 5e-
0; Mismatches
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             r is capable of ous nucleic acid in both monocot
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Best Local 9
       The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions: The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and dicot plant species, and therefore can be readily applied to a variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altere
                                                                                                                                                                                      Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric expression promoter;
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                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                   Rance
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                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; intergenic region; Commelina yellow mottle virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Commelina yel
Cassava vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                    Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric expression
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                                                                                                                                                                                                                                                                                                                                                                                                                      mosaic virus.
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ter; Cassava
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                                                                                                                                                                                                                                                                           Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimeric expression promoter; plant vascular expression plant green tissue expression promoter; Cassava vein mon transgenic plant; chimera; ss.
                                                                                        a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Commelia
Chimeric - Cassava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of chimeric expression promoter MPr1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001
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             Local
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les 62; Conserv
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                                                                                                                                                                                                                                           5
ch 100.0%; l Similarity 100.0%; 62; Conservative 0
                                                                                                                                                                                                                                          Page 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 BP; 107
                                                                                                                                                                                                                                                                                                                                                              Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative (
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                                                                              transgenic plants.
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                                                      122
                                                                                                                                                                                                                                        91pp;
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Score 62; DE
Pred..No. 7.3
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Pred. No. 7e-
D; Mismatches
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 7.3e-12;
hes 0;
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                          DB 21; Length 371;
                                                      0
                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pression promoter; vein mosaic virus
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RESULT 5
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                                                                       Matches
                                                                               Query Match
Best Local (
                                                                                                                                                                                                           This sequence represents a cassava vein mosaic virus promoter, and is a nucleic acid molecule of the invention. The promoter is capable of initiating transcription of an operably linked heterologous nucleic acid sequence in a plant cell. The csVMV promoters are active in both monocol and dicot plant species, and therefore can be readily applied to a mid dicot plant species, and therefore can be readily applied to
                                                                                                                                                   variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altered
                                                                                                                                                                                                                                                                                                                      Cassava vein mosaic virus
DNA sequences for producir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassava vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cassava vein mosaic virus; CsVMV; promoter; cultivated crop; tissue-specific expression control; transgenic plant; ss.
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                                                                                                                   Sequence 392
                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                           phenotype(s)
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                                                                                                                                                                                                                                                                                                                                                                               Beachy RN,
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                                              1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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                        GAAGATAAGGTCGGTGA'
                                                                                                                                                                                                                                                                                     2; Page 74; 115pp;
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 62
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                                                                               Similarity
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                                                                       Conservative
                                                                                                                   BP; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US10376
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                                                                                                                                                                                                                                                                                                                   ic virus promoter producing transge
                                                                                100.0%;
                                                                                                                  A; 64
                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                               Fauquet C,
                                                                                                                   Ç
                                                                                                                                                                                                                                                                                                                      romoter - used to express
transgenic plants having
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                                                                                Score
Pred.
                                                                                                                    83
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                                                                    e 62; DB 19;
. No. 7.3e-12;
smatches 0;
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altered
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Nucleotide sequence of chimeric expression promoter MPr1162.
                               19-PEB-2001
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; chimera; ss.
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                                                            AAA96853;
                                                                                          AAA96853 standard; DNA; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 86; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2000; 2000WO-IB00370
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                                                                                                                                                                    195
                                                                                                                                                                                                                               135
                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                producing transgenic plants.
                                                                                                                                                                                                 AG
                                                                                                                                                                                                                                                  GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTCGAAAATGTA 60
                                                                                                                                                                    AG 196
                                                                                                                                                                                                                                GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAAATGTA 19
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                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99FR-0003925
                                                                                                                                                                                                                                                                                                                                                    127 A; 80 C; 87 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392
                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                        Score 62; DB 21;
Pred. No. 7.3e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    98 T;
                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                    Length 392;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                             RESULT 8
AAV14021
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZXSXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                     문
                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
Chimeric -
                                                                                                   CsVMV promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic plant; chimera; ss.
 WO9748819-A1
                              Cassava vein mosaic virus
                                                        tissue-specific expression
                                                                                                                                    18-JUN-1998
                                                                                                                                                                  AAV14021;
                                                                                                                                                                                                 AAV14021 standard; DNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200058485-A1
                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                           195 ÅG 196
                                                                                                                                                                                                                                                                                                      61 AG
                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 128
                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 75 C;
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The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commellina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric expression promoter for transgenic plant production, or sequence from promoter comprising vascular expression region rewith sequence from promoter comprising green tissue expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promplant green tissue expression promoter; Cassava vein mosaic
Cassava vein mosaic virus; CsVMV; promoter; cultivated crop; tissue-specific expression control; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAGATAAGGTCGGTGATTGTGAAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 85; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theisen M;
                                                                                                                                                                                                                                                                                                       BP.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; DB 21;
No. 7.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 T; 0 other;
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RESULT 9
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AC AAV1
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a cassava vein mosaic virus promoter, and is a nucleic acid molecule of the invention. The promoter is capable of initiating transcription of an operably linked heterologous nucleic acid sequence in a plant cell. The CsVMV promoters are active in both monocot and dicot plant species, and therefore can be readily applied to a variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression in a tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altered
                           Beachy RN,
                                                                                                                                                                                                                                                                                                                                                                 Cassava vein mosaic virus;
tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                        CsVMV promoter pdeltaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV14026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phenotype(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassava vein mosaic virus promoter - DNA sequences for producing transgeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1997.
                                                                                                                                                                                                                                                                    WO9748819-A1
                                                                                                                                                                                                                                                                                                                 Cassava vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV14026 standard; DNA; 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1996;
                                                                                                                                                                      20-JUN-1997;
                                                                         (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%;
1 Similarity 100.0%;
62; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                           Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
                                                                                                                                                                                                                                                                                                                 mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                         Kochko A,
                                                                                                                      96US-0020129
                                                                                                                                                                      97WO-US10376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kochko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 60 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
                         Fauquet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fauquet
                                                                                                                                                                                                                                                                                                                                                               CBVMV; promoter; cultivated crop; control; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         romoter - used to express heterologous transgenic plants having altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ი</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verdaguer
                         Verdaguer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 10
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a cassava vein mosaic virus promoter, and is a nucleic acid molecule of the invention. The promoter is capable continitiating transcription of an operably linked heterologous nucleic ac sequence in a plant cell. The CSVMV promoters are active in both monoc and dicot plant species, and therefore can be readily applied to a variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression in tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altered
                                                                                                                                                                                                                                                                                                                   Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic transgenic plant; chimera; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cassava vein mosaic virus promoter - used to express DNA sequences for producing transgenic plants having
                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 420
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                                    sequence from with sequence
                                                                                                                  Rance I,
                                                                                                                                                                      29-MAR-1999;
                                                                                                                                                                                                29-MAR-2000;
                                                                                                                                                                                                                            05-OCT-2000.
                                                                                                                                                                                                                                                     WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of chimeric expression promoter MPrl163
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA96854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA96854 standard; DNA; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phenotype(s)
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                                                                                                                                             MERISTEM THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                 expression promoter for transgenic plant production, compris
from promoter comprising vascular expression region replaced
uence from promoter comprising green tissue expression region
                                                                                                                  Gruber V,
                                                                                                                                                                                                                                                                                Cassava
                                                                                                                                                                                                                                                                                             Commelina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 149
                                                                                                                                                                                                  2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                      99FR-0003925
                                                                                                                                                                                                                                                                               vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                             yellow mottle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 65
                                                                                                                  Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                    vein mosaic virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterologous
altered
                                                                                                                                                                                                                                                                                                                                                promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Claim 5; Page 86; 91pp; English.

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RESULT 11
AAV14053
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Matches
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      This sequence represents a cassava vein mosaic virus promoter, and is a nucleic acid molecule of the invention. The promoter is capable of initiating transcription of an operably linked heterologous nucleic acid sequence in a plant cell. The CSWMV promoters are active in both monocot and dicot plant species, and therefore can be readily applied to a variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression in a tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic regions.
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 87; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cassava vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue-apecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cassava vein mosaic virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CsVMV promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV14053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV14053 standard; DNA; 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-063157/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       nosaic virus promoter -
for producing transgeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kochko A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0020129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fauquet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CsVMV; promoter; cultivated crop;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       romoter - used to e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No. 7.6
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verdaguer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6e-12;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       express heterologous
s having altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 462;
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Query Match Best Local (

Similarity

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Score Pred.

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Matches

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Best Local :
                                                                                                                                                                                                                           Chimeric expre
sequence from
with sequence
                       The present sequence represents a promoter fragment from the intergenic region of Cassava vain mosaic virus. The promoter is used to construct chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. The chimeric promoters are useful for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter; intergenic region; chimeric expression promoter; plant green tissue expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 476
                                                                                                                                                                                     Claim 4; Page 80; 91pp; English
                                                                                                                                                                                                                                                                                       WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                   Rance
                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA96836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96836 standard; DNA; 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phenotype
                                                                                                                                                                                                                                                                                                                                               (MERI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                             MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                          expression promoter for transgenic plant production, compris-
from promoter comprising vascular expression region replaced
uence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intergenic region; Commelina yellow mottle virus; expression promoter; plant vascular expression promoter; en tissue expression promoter;
                                                                                                                                                                                                                                                                                                                Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intergenic region of Cassava vein
                                                                                                                                                                                                                                                                                                                                                                          99FR-0003925
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vein mosaic virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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AAFSSULT 13
AAFSS 1D
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AC AAFSS
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                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a region which is immediately 5' to the Cassava vein mosaic virus (CsVMV) translational start site. The sequence is used as an enhancer domain in cassettes of the invention. The specification describes an enhancer cassette comprising a duplicated enhancer derived from CsVMV. It can be operably linked to a nucleic acid, the expression of which confers herbicide resistance, fungal, bacterial disease resistance or insect resistance and regulates plant ripening, degradation, colour and sweetness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancer cassette which forms an promoter useful for manipulating duplicated enhancer derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu D,
   AAV14020;
                                      AAV14020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-211307/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tungal
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ripening; plant
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                                      standard; DNA; 524
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                                                                                                                                                                                                                                                                                                                                                 198 A;
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Pred. No. 7.8e-12;
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                                                                                                                                                                                                                                                                                                                                                   129 T; 0 other;
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RESULT 15
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Best Local
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Cassava vein mosaic virus
                                    tissue-specific expression
                                                         Cassava vein mosaic virus;
                                                                                              CsVMV promoter
                                                                                                                                                                              AAV14018;
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                                      CsVMV; promoter; cultivated crop; control; transgenic plant; ss.
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Best Local Similarity 100.0%; 1
Matches 62; Conservative 0;
                                                                                                                                                                                                                                                                                            This sequence represents the cassava vein mosaic virus promoter pA, and is a nucleic acid molecule of the invention. The promoter is capable of initiating transcription of an operably linked heterologous nucleic acid sequence in a plant cell. The CsVMV promoters are active in both monocot and dicot plant species, and therefore can be readily applied to a variety of cultivated crops. Although generally constitutive, the derivative promoters include promoters that can regulate expression in a tissue-specific manner, and therefore are useful for controlling expression of heterologous genes in a tissue-specific manner. The promoters can be used for producing transgenic plants with an altered phenotype.
                                                                                                                                                                                                                                                                  Sequence 526 BP; 202 A; 80 C; 111 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassava vein mosaic virus promoter - used to express heterologous DNA sequences for producing transgenic plants having altered phenotype(s)
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AXO36744 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS		C 44 45	43	4. 4	40	c 38	. w	15 15 15 15 15 15 15 15 15 15 15 15 15 1	ມເມ	c 32	30	28 29	26 27		0 0 0 0 0 0	c 22	่งเ	19 19	c 17	15	13 14	12	10 11	9 (8 7	o,	4.10	. ω	· 2	Result No.
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synthetic construct
artificial sequences.
1 (bases 1 to 317)
Rance, I., Thetsen, M. and Gruber, V.
Chimeric expression promoters originating fromottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 3 05-OCT-2000;
MERISTEM THEARPEUTICS (FR); RANCE IANN (FR)
; GRUBER VERONIQUE (FR)
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synthetic construct.
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1 (bases 1 to 371)
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Sequence 5 from Patent WO0058485
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AX036737
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 392)
Rance, I., Theisen, M. and Gruber, V.
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating fromottle virus and cassava vein mosaic virus patent: WO 0058485-A 21 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); GRUBER VERONIQUE (FR)
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/db xref="taxon:32630"
/note="promoter MPr1164"
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/db xref="taxon:32630"
/note="promoter MPr1146"
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1 (bases 1 to 462):
Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 20 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
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Rance, I. Theisen, M. and Gruber, V.
Chimeric expression promoters originating f
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-007-2000;
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/db_xref="taxon:32630"
/note="promoter MPr1163"
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/db_xref="taxon:32630"
/note="promoter MPr1162"
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Pred. No. 1.5e-10;
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Cassava vein mosaic virus
Viruses; Retroid viruses; Caulimoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 515)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus Patent: WO 0059485-A 2 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2
AX036736
                                                                                                                                                                                                                                Duplicated cassava vein mosaic virus Patent: WO 0114573-A 1 01-MAR-2001;
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                                                                                                                                                                                                                                                        1 (bases 1 to 515)
Xu,D. and Nielsen,M.T.
                                                                                                                                                                                                                                                                                   Viruses
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                                                                                    Conservative
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                                                                                                                                                                                                                       Inc.
                                                                                                                                            /db_xref="taxon:38062"
/note="based on cassava vein
78 c 110 g 129 t
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Promoter from the intergenic region of Mosaic Virus of 515 bp in length EMBL U59751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="synthetic construct"
db_xref="taxon:32630"
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                                                                                                                                                                                 organism="Cassava vein mosaic virus"
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from Patent WO0058485.
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79 c
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                                     GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACATGTAAGGTGGAAAATGTA 317
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Barbas, C.F., Srege, J.T., Guan, X. and Dalmia, B.
Methods: and compositions to modulate expression in plants
Patent: WO 0152620-A 1 26-JUL-2001;
The Scripps Research Institute (US); SYNGENTA AGRICULTURAL
DISCOVERY, INC. (CA)
                                                                                                                                                                                                                                       Duplicated cassava vein mosaic virus enhancers Patent: WO 0114573-A 3 01-MAR-2001;
                                                                                                                                                                                                                                                                1 (bases 1 to 593)
Xu,D. and Nielsen,M.T.
                                                                                                                                                                                                                                                                                                      synthetic construct
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                                                                                                                                                                                                                              Profigen Inc. (US)
                                                                                                                                                                                                                                                                                                                 synthetic construct.
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ilarity 100.0%;
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/db xref="taxon:32630"
/note="based on cassava vein mosaic
86 c 135 g 144 t
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/db_xref="taxon:32630"
/note="Promoter CsVMV"
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Pred. No. 1.5e-10;
Mismatches 0;
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AX036756
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BASE COUNT 296
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                                                                                                                                                                        1 (bases 1 to 838)
Lamberty, M., Hofmann, J., Bulet, P. and Brookhart, G.L.
Gene coding for heliomicine and use thereof
Patent: WO 9953053-A 19 21-CCT-1999;
LAMBERTY MIREILLE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)
                                                                                                                                                                                                                                                                                                                                 Sequence 19 from Patent Ax014764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FE; GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 600)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 from Patent AX036756
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/db xref="taxon:32630"
/noTe="promoter MPr1165"
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/db_xref="taxon:32630"
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AX088389
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Sequence 2 from Patent W00114573.
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Sequence 4 from Patent WO0114573.
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Sequence 2	Sequence 2	Sequence 2	Sequence 1	Sequence 3	Sequence 5	Sequence 1	Sequence 1	Sequence 3	Patent No. 5208144	Sequence 4	Sequence 1	Sequence 3	Sequence 6	Sequence 1	Sequence 8	Sequence 8	Sequence 6
23, Apr	23, App	23, App	l, Appl	3, Appl	5, Appl	l, Appl	1643, Ap	 Appli 	520814	4, Appl	19, App	3, Appl	61, App	l, Appl	3, Appl	3, Appl	5, Appl

ALIGNMENTS

Sequence 44, Applia Patent No. 5948650 APPLICATION NUMBER: PCT/JP96/02121 PILING DATE: 26-JUL-1996 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: JP HEI 7-211328 FILING DATE: 28-JUL-1995 PRIOR APPLICATION NUMBER: JP HEI 8-130586 FILING DATE: 30-APR-1996 ATTORNEY/AGENT INFORMATION: NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24618 REFERENCE/DOCKET NUMBER: 2589-057-0PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000 GENERAL INFORMATION: TELEFAX: (703) 413-2220 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, V CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/809,297 FILING DATE: 06-MAY-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICANT: ARAKI, SHIGEKI APPLICANT: TSUCHIYA, YOHICHI TITLE OF INVENTION: GENERIC VARIETY IDENTIFYING METHOD TITLE OF INVENTION: HOPS CORRESPONDENCE ADDRESS MOLECULE TYPE: STATE: V LENGTH: 629 base pairs TYPE: nucleic acid STRANDEDNESS: double STRANDEDNESS: TOPOLOGY: li STREET: 1755 SOU CITY: ARLINGTON ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. 22202 ٧ Application US/08809297 3: P.C. 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400 USA linear DNA (genomic) 2589-057-0PCT Version #1.30

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CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
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NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION:
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FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 99117
OTHER INFORMATION:
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LOCATION: 90842
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LOCATION: 88073
OTHER INFORMATION:
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LOCATION: 72794
OTHER INFORMATION:
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LOCATION: 103806
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OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: pol:
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LOCATION: 134134
OTHER INFORMATION:
 OTHER INFORMATION:
             NAME/KEY: allele
LOCATION: 93690.
                                              LOCATION: 90819..9
OTHER INFORMATION:
                                                                                            OTHER INFORMATION:
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LOCATION: 90819..90865
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LOCATION: 88050..88096
OTHER INFORMATION: pol
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LOCATION: 72771..72817
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LOCATION: 72771..72817
OTHER INFORMATION: pol:
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LOCATION: 150329
OTHER INFORMATION:
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LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 134374
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LOCATION: 134362
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LOCATION: 108106
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OCATION: 146345
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OCATION: 108308
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OCATION: 160031
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                                                          90819..90865
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polymorphic fragment 5-128-60 SEQ ID32
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50

NAME/KEY: allele

OCATION: 97099

..97145

LOCATION: 93690..93736

INFORMATION: polymorphic fragment 5-128-60 SEQ ID53

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                            Matches
                                                   Query Match
                                                                                                NAME/KEY: allele
LOCATION: 108127..1
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic
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LOCATION: 97099..97145
OTHER INFORMATION: pol;
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LOCATION: 103783..103828
DIHER INFORMATION: polymo
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LOCATION: 99075..99121
OTHER INFORMATION: pol
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LOCATION: 99075..99
OTHER INFORMATION:
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DTHER INFORMATION:
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LOCATION: 108127.
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OTHER INFORMATION:
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LOCATION: 106918..106966
DTHER INFORMATION: polymo
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LOCATION: 99094..99140
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OCATION: 108084..108130
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OCATION: 106918.
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OTHER INFORMATION: polym
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OCATION: 99094..99140
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                         Score 24.8; Di
Pred. No. 16;
1; Mismatches
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RESULT 4
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US-08-910-925-2
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                                      Sequence 207, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
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                                                                                                                                                                                                       Matches
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Best Local Similarity
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
          APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN NUMBER OF SEQUENCES: 4
                                                                                                                                              949
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CTTY: Palo Alto
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LIBRARY: FILL
ONE: 53219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                     39.4%;
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            Streptococcus pneumoniae
 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/910,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PININ SPLICE VARIANT
                                                                                                                                                                                                      Score 24.4; D
Pred. No. 8;
0; Mismatches
                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ន
                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                      21;
             Polynucleotides and
                                                                                                                                                                                                                                 Length 2369;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                      0
                                                                                                                                                                                                       Gaps
            Sequences
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US-08-182-175A-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.3
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/08182175A Patent No. 5559223
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2616 GAAGATCAAGTTAGGGATTATGCAAGAGAAGTATAGGCTTTAATGAAGTTGAAGAA 2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: * Brookes, A. Anders
REGISTRATION NUMBER: 36,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 PPLICANT: Janet A. Rice
                                                                                                                                                                                                                              STREET: 1007 Mar.
                                                        CLASSIFICATION:
                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                         COMPUTER: Macintosh
OPERATING SYSTEM: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/961,527 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                        19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                     Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B: Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3454 base pairs
                                                                                                                                                                                                                                               2: E.I. du Pont de Nemours and Company 1007 Market Street
                                                                                                                                                                                                                                                                                                                                  Sharon J. Keeler
                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                   Saverio Carl Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (301) 309-8512
(301) 75 NO: 207:
                                                                                                             Microsoft Word, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309-8504
                                                                                                                             Macintosh System,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSDOS version 6.2
                                                                                    US/08/182,175A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                               6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3454;
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PCT-US92-06412-100
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                                                                                                                                                                                                        Wilmington
: Delaware
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                                                                                                                                                                                                                                                               19898
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                                                                                                                                                                                                                                                                             USA
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,692
REFERINCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 3..116
OTHER INFORMATION:
OTHER INFORMATION:
11 GAAGATGAAAAAGCTCAAGGAGGAAATGGCTAAGATGAAAGACGAAATGTGGAAACTGAA 70
                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                  1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linda Axamethy Floyd
                                                                                                                                                                                                                                                                                                                                                                                                  130 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (302) 892-7949
                                                                      Conservative
                                                                                                                                                                                                                                                                               DH5 alpha
                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    double
                                                                                    38.1%;
61.3%;
                                                                                                                                                       /standard_name= "SSP-seg5"
                                                                                                                                                                        /function= "synthetic storage protein
/product= "protein"
/gene= "ssp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                      100:
                                                                  Score 23.6; Di
Pred. No. 7.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB-1031
                                                                                                     DB 1;
                                                                      24;
                                                                                                     Length 130;
                                                                      Indels
                                                                      <u>.</u>
                                                                      Gaps
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ILT 6
US92-06412-100
US92-06412-100

GUENCE 100, Application PC/TUS9206412

ENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler

APPLICANT: Janet A. Rice

TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing

NUMBER OF SEQUENCES: 113

ADDRESSEE E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STRATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER ERADABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATION SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
              INFORMATION FOR SEQ ID NO:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
PILLING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: 1
ORIGINAL SOURCE:
STRAIN: E, co.
                                                                     NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word, 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sharon J. APPLICANT: Janet A. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBER OF SEQUENCES:
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OTHER INFORMATION:
                                         TELEFAX:
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                           19898
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                                                                                                                                                                                                                                                                                                                                                                                       Wilmington .
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                                                                                                                                                                                                                                                                                                                                                                                                    3: E.I. du Pont de Nemours and Company
1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08182175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 base pairs
                                             (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Janet A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saverio Carl Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                         Macintosn
                                                           (302) 992-4929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice
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61.3%;
                                                                                                                                                                                                                                                                        Macintosh System, 6.0
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/gene= "ssp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function= "synthetic storage protein
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER
APPLICATION NUMBER

APPLICATION NUMBER

TO THE PROPERTY APPLICATION NUMBER

                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                              NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: 1
                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 9 August 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                 TELEPHONE: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GAAGATGAAAAAAGCTCAAGGAGGAAATGGCTAAGATGAAAAGACGAAATGTGGAAACTGAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: E.
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/743,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Macinto
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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                                ENGTH:
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   NUCLEIC
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340 base pairs
UCLEIC ACID
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1007 Market Street
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E: DH5 alpha
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Janet A. Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application PC/TUS9206412
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/product= "protein"
/gene= "ssp"
/standard_name= "SSP-534"
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Pred. No. 9.7;
0; Mismatches
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; Sequence 687, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                      APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
APPLICATION ODDEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
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itent No. 6444799
                                                                                                                                                                                                                                                                                   CLASS" - DATE: 73
        NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                  PRICE APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PP2911
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 31-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGGACACATGTAAGGTGGAAAATGTA 60
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650-813-5600
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                                                                                                         PCT/AU98/01023
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                                                                                                                                                                                                                                                  PP1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function= "synthetic seed storage protein"
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/gene= "ssp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.6; DB Pred. No. 9.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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US-08-809-297-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 43,
                                                            TELEFAX: (703) 413-22
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     FILING DATE: 28-JUL-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-APR-
                                                                                                                                                                                                                                                                                       CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PCT/JP96/02121
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ORIGINAL SOURCE:
ORGANISM: POR
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                                                                                                       REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
STRANDEDNESS:
                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 26-JUL-1996
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1755 SOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAA 55
                           ENGTH:
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5948650
           : 599 base pairs nucleic acid
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1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
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TSUCHIYA,
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                                                                                          (703)
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GENETIC VARIETY IDENTIFYING METHOD IN
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Pred. No. 1
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TOPOLOGY:

linear

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                                                                                                                             ; PUBLICATION DATE: US-08-098-327E-33
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Best Local Similarity 67.3%;
Matches 33; Conservative
                                                                             Query Match
Best Local Similarity
                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GUERIN-THAN APPLICANT: DRUILHE, TITLE OF INVENTION:
                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PUBLICATION INFORMATION:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 464 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
151 GAAGAAAAAGTTGAAGAAAGTGTĀGAĀGĀAĀATGĀCGĀAGAĀAĞTGTAGAAGAAATGTA 210
                                                                                                                                                                                                                                                                                                                                                         NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Polonia
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                                                                                                                                                             DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 24-NOV
                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                              1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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                                                               Conservative
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                                                                                                                                                                                                                                                                                                                       (703)
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                                                                                                                                                                                                                                                                                    836-2021
NO: 33:
                                                                                                                                                             WO 92/13884
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                                                                              37.4%;
61.7%;
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                                                                                                                                            20-AUG-1992
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....er: 010830-045
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Pred. No. 14
                                                              Mismatches
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RESULT 12 . US-08-462-625-33

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US-09-641-638-575
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                                                                                                                                                                                  Sequence 575, Appl
Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                           Best Local
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1 CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                APPLICANT:
                                                                                                                                                 APPLICANT:
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APPLICATION NUMBER: US 08/098,327
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PUBLICATION INFORMATION: DOCUMENT NUMBER: WO 92/138
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TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 836-6620
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                   1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION DATE:
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                                                                                                                                                                    INFORMATION:
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                                                                                           Cohen, Annick
                                                                                                           Bougueleret, Ly
Chumakov, Ilya
                                                                                                                                                   Blumenfeld, Marta
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20-AUG-1992
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PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent pm
SEQ ID NO 575
LENGTH: 1001
TYPER TWO

TYPE: DNA ORGANISM: Homo Sapiens

EATURE:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: FILING DATE: 1999-0 APPLICATION NUMBER:

1999-05-07

US 60/133,200 US 09/275,267

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US-08-973-462-3
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; LOCATION: 888
; OTHER INFORMATION: n=a, g, c or
US-09-641-638-575
                                                                                                                                  US-08-973-462-3
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LOCATION: 214
OTHER INFORMATION: 10-234-179 : deletion AA
NAME/KEY: misc_binding
LOCATION: 195..213
OTHER INFORMATION: 10-234-179.misl
NAME/KEY: primer_bind
LOCATION: 36..56
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 346..366
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EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
ENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1891)
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: P. falciparum
                                                                                                                                                                                                                                           LENGTH: 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 61.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 37.4%; Local Similarity 61.7%; es 37; Conservative
1 GAAGATAAGGTCGGTGATTGTGAAAGAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
                                                                      37.4%;
61.7%;
                                                      Score 23.2; DB 4;
Pred. No. 20;
0; Mismatches 23;
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Pred. No. 17
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                                                        23; Indels 0;
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; TYPE: DNA
; ORGANISM: P. falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5361)
US-08-973-462-2
Search completed: May 11, 2003, 03:07:35
Job time : 53.8622 secs
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US-08-973-462-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MALARIAL PRIFILE REFERENCE: 0660-0125-0 PCT
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                                                                                               670 GAAGAAAAGTTGAAGAAAGTGTAGAAGAAAATGACGAAGAAAGTGTAGAAGAAAATGTA 729
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Maximum DB seq length: 2000000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07
2: /cgn2_6/ptodata/2/pubpna/PCT_
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_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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6/ptodata/2/pubpna/US10 NEW PUB.seq:*
6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
6/ptodata/2/pubpna/US0_NEW_PUB.seq:*
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US-09-963-803-10
US-09-963-803-3
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US-09-963-803-22
US-09-963-803-22
US-09-963-803-22
US-09-963-803-26
US-09-963-803-26
US-09-963-803-4
US-09-963-803-2
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US-09-963-803-2
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US-09-963-803-2
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Million cell updates/sec
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Sequence 3, Appli
Sequence 5, Appli
Sequence 21, Appl
Sequence 19, Appl
Sequence 20, Appl
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Sequence 1, Appli
Sequence 22, Appl
Sequence 4, Appli
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37.4 37.4 37.4	37.7 37.7	38.1 38.1 38.1	38.7 38.4	39.4 38.7	39.7 39.4	40.6	41.0 41.0	41.9	41.9 41.9 41.9
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US-09-837-344-33 US-09-938-842A-2126 US-09-974-300-2651	US-09-764-891-1302 US-09-938-842A-3993	US-09-764-898-59 US-09-764-898-109 US-09-764-898-131 US-09-790-988-1	US-09-918-995-17393 US-09-918-995-28694	US-09-822-849A-1 US-09-878-574-13995	US-09-880-107-3030 US-09-925-300-416	US-10-091-504-1634 US-09-764-869-1634	US-09-770-149-403 US-10-278-173-119	US-09-870-130-1 US-09-834-975-999	US-09-860-670-34 US-09-764-853-115 US-10-160-501-12 US-10-160-501-13 US-09-870-130-3
Sequence 33, Appl Sequence 2126, Ap Sequence 2651, Ap	30	Sequence 59, Appl Sequence 109, App Sequence 131, App Sequence 1, Appli	Sequence 17393, A Sequence 28694, A	Sequence 1, Appli Sequence 13995, A	Sequence 3030, Ap Sequence 416, App	Sequence 1634, Ap Sequence 1634, Ap	Sequence 403, App Sequence 119, App	Sequence 1, Appli Sequence 999, App	34, e 11, e 3,

ALIGNMENTS

RESULT 1 US-09-963-803-10

Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:

Application US/09963803

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PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEO ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 62
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: TUPORAGETTINE
                RESULT 2
US-09-963-803-3
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Best Local Similarity
Matches 62; Conserve
; Sequence 3, Application US/09963803.
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CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow :
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Directional desoxynucleotide building block OTHER INFORMATION: S3
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61 AG
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                                                                                                                                                                                                                                                                                                                                          SOFTWARE: I
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Best Local Similarity 100.0%;
Matches 62; Conservative 0
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OTHER INFORMATION:
-09-963-803-3
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                                                                                                                                     -09-963-803-5
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                    NAME/KEY: promoter LOCATION: (1)..(371) OTHER INFORMATION:
                                                                                                                                                                                                                                     OTHER INFORMATION: promoter MPr1146
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OTHER INFORMATION: Promoter MPr1116
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ORGANISM: Artificial Sequence
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                                                                    Local Similarity
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1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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Pred. No. 3.8e-12;
); Mismatches 0;
                                                                    Score 62; DB 9; Length 371; Pred. No. 4e-12;
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Best Local Similarity 100.
62; Conservative
                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 19
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Publication No. US20030028922A1
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Publication No
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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TITLE OF INVENTION: Chimeric expression promoters originating
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                         PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR TILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT 1B00/00370
PRIOR FILING DATE: 2000-10-05
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PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT 1B00/00370
PRIOR FILING DATE: 2000-10-05
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CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                     FILE REFERENCE: 184332042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 39
                     ORGANISM: Artificial Sequence FEATURE:
                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: promoter MPr1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
OTHER INFORMATION: promoter MPr1162
                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EATURE:
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PRIOR APPLICATION NUMBER: 7001-9-26

PRIOR PILING DATE: 2001-9-26

PRIOR PILING DATE: 199-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOPTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 462

Type: no.
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US-09-963-803-2
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US-09-963-803-20
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; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
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              Sequence 2, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapuetics

TITLE OF INVENTION: Chimeric expression promoters originating:

TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 18433042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 62; DB 9; I Best Local Similarity 100.0%; Pred. No. 4.2e-12; Matches 62; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: promoter LOCATION: (1)..(393) OTHER INFORMATION:
PRIOR APPLICATION NUMBER: FR 99/03925
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                                                                                                                                                                                                                                                                                   195 AG
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Pred. No. 4e-12;
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US-09-765-555-1
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LENGTH: 515
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No. US20030037355A1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PASESEQ for Windows Version 4.0
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NAME/KEY: promoter
LOCATION: (1)..(515)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods and compositions TITLE OF INVENTION: expression in plants FILE REPERENCE: 27801-20014.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/620,897 PRIOR FILING DATE: 2000-01-21
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                                                                                                                                                                                                                                            LENGTH: 532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                     273 GÁAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 332
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                                 61 AG 62
                                                                                        1 GAAGATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 60
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                                                                                                                                         100.0%; Score 62; DI
100.0%; Pred. No. 4.3
tive 0; Mismatches
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hes 0;
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US-09-963-803-22 ; Sequence 22, Application US/09963803 ; Publication No. US20030028922A1

RESULT 9

GENERAL INFORMATION:

GENERAL INFORMATION:

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US-09-847-057-4/C
; Sequence 4, Application US/09847057
; Patent No. US20020004943A1
; GENERAL INFORMATION:
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                                         RESULT 11
US-09-874-926-4/c
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; Sequence 4, Application US
7-Patent No. US20020010950A1
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; SEQ ID NO 22
; LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4
SOPTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                               Matches 62;
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Best Local (
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: Virus and Cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
FRIOR APPLICATION NUMBER: FR 99/03925
FRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PRIOR 1100 DATE: 2000-10-05
RIOR APPLICATION NUMBER: PRIOR 1100 DATE: 2000-10-05
RIOR APPLICATION NUMBER: PRIOR 5100 DATE: 2000-10-05
RIOR FILING DATE: 2000-10-05
RIOR FILING DATE: 2000-10-05
RIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: AGRINOMICS, LLC.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLANFILE REFERENCE: PAGODA
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Binary vector pAGI4002
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OTHER INFORMATION: promoter MPr1165
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                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 10; llarity 100.0%; Pred. No. 8.2e-12; Conservative 0; Mismatches 0;
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                     US/09874926
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Pred. No. 4.5e-12;
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; LENGTH: 12241
; TYPE: DNA
; ORGANISM: PAG2370
US-10-033-190-5
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US-09-963-803-7
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US-10-033-190-5/c
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                                                                                                                       Sequence 7, Application US/09963803 Publication No. US20030028922A1 GENERAL INFORWATION:
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Best Local Similarity 100.
55.7 62; Conservative
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IITLE OF INVENTION: Identification and characterization of a curly phenotype FILE REFERENCE: curly

CURRENT APPLICATION NUMBER: US/09/874,926

CURRENT FILING DATE: 2001-06-05
                                                                APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Exelixis Plant Sciences, TITLE OF INVENTION: IDENTIFICATION TITLE OF INVENTION: TOMATO FILE REFERENCE: EPO1-002C
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SOFTWARE: PatentIn version 3.0
               FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: FR 99/03925
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ORGANISM: pAGI4002
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100.0%; Pred. No. 9e-12;
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Pred. No. 8.2e-12;
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AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
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LOCATION: (1)..(348)
OTHER INFORMATION:
US-09-963-803-4
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                                                                                                                                       Query Match
Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
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Publication No. US20030028922A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
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PRIOR PELICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Meristem Therapuetics
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: promoter MPr1154
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ORGANISM: Artificial Sequence
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                                                                    167 GAAGATAAGGTCGGTGATTGTG-AAGAGACATAGAGGACACATGTAAGGTGGAAAATGTA 225
226 ÁG 227
                                 61 AG 62
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ilarity 98.4%;
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98.4%;
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Pred. No. 5.1e-08;
Pred. No. 5.1e-08;
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Pred. No. 4.9e-08;
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RESULT 15

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Search completed: May 11, 2003, 06:11:41 Job time : 64.3784 secs
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LENGTH: 398
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow:
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: promoter LOCATION: (1)..(398) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 184332042
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: promoter MPr1147
                                                                                 276 AG 277
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Pred. No. 5.3e-08;
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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220:
221:
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24:
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27:
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62
1 gaagataaggtcgg!
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	28	28.8	28.8	28.8	28.8	29	No. Score	
	45.2	46.5	46.5	46.5	46.5	46.8	Query Match	of
	214	585	576	548	359	699	Query Match Length DB ID	
	17	12	9	12	12	17	DB :	
	AZ484766	BG280606	AI399593	BG279526	BG278522	AQ156245	Length DB ID	
٠	AZ484766 1M0311P23	BG280606 c5b03np.f	AI399593 NCSP6F6T7	BG279526 b3g07np.f	BG278522 a5c01np.f	AQ156245 nbxb0005D	Description	

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BG281521 BG71815 BE263319 BE26535 BE296505 BU008674 BQ114742	AV697865 BG699782 BE269715 BU002041	AA436699 AAQ43893 AW958726 AQ687904 BF590238 BF109238 BF1034799 BF0034799 BH446500	BM360131 AJ435435 AZ827513 BQ458384 BBG458386 BB602510 N70246 B14130 AQ350013 AA442502	AQ165808 AQ212331 BG279968 BB726034 AZ570132 AQ410127 AQ620909 FR0020027 CNS03WUW BF622523
1521 5815 9319 5505 8674 1742	97865 AV697865 99782 60268148 99715 60118587 02041 QGG30A15	HS 5065 HS 5065 EST3707 nbxb007 nab21g0 7157d11 Fugu ru Fugu ru Fugu ru Fugu ru	HM360131 GA EAGUZ AJ435435 AJ435435 AZ435435 AZ435435 AZ827513 2M0104B03 BQ459384 HA05F23x BB602510 HVSMEh009 N70246 Za57b09.91 B14110 A-929H3.TP AQ350013 RPCI11-11 AA442502 zv59c01.r	HS 3071 HS 2240 b7h08np. 60156132 260156132 700000 HS 5083 HS 2178 F. rubrip F. rubrip Tetraodo

ALIGNMENTS

FEATURES	TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	RESULT 1 AQ156245 LOCUS DEFINITION ACCESSION VERSION VERSION
CONTACT: WING KA Clemson University Genomics Institute Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GGAAACAGCTATGACCATG Class: BAC ends High quality sequence stop: 394. Location/Qualifiers	A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998) On Sep 10, 1998 this sequence version replaced gi:3552334.	Oryza sativa. Oryza sativa Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza. 1 (bases 1 to 699)	AQ156245 699 bp DNA linear GSS 12-SEP-1998 nbxb0005D02r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0005D02r, DNA sequence. AQ156245 AQ156245.1 GI:3592027

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JOURNAL COMMENT
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AUTHORS
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Fax: 405 320 Email: broe@ou.edu
Email: broe@ou.edu
Contact Dr. Mary Anne Nelson, Department
New Mexico, Albuquerque, NM 87131 (e-mail address
regarding clone availability
Seq primer: M13 Universal Forward Primer
Seq primer: M13 Universal Forward Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a5c0lnp.fl Neurospora crassa sexual cDNA library, Uni-zap vector system Neurospora crassa cDNA clone a5c0lnp 3', mRNA sequence. BG278522
                                                                                                                                                                           620 Parrington Oval,
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                 Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, U
620 Parrington Oval, Norman, OK 73019, U
                                                                                                                                                                                                                                                                              Other_ESTs: a5c0lnp.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                     Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 359)

Kupfer, D., Lai, H., Nelson, M. and Roe, B.
                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                 ESTS from a Neurospora crassa Sexual cDNA Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4530"
/clone="nbxb0005D02r"
/clone_lib="CUGI Ride BAC I
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Tab host="K. GOLI PALAVE" note="Vector: pBeloBACII; Site 1: HindIII; Site 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa"
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Pred. No. 1.1e+02;
D; Mismatches 20;
                                                                                                            Department of Biology, University of 7131 (e-mail address manelson@unm.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC Library
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ORGANISM
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACGGGCAGTGACAGAGAAAGAGAAATAAAGGAGACAGGTAAGGGGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG279526 TRIA LINEAR EST 21-FEB-20 b3907np.fl Neurospora crassa sexual cDNA library, Uni-zap vector system Neurospora crassa cDNA clone b3g07np 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 548)
Kupfer, D., Lai, H., Nelson, M. and Roe, E
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact Dr. Mary Anne Nelson, Department of Biology, University of New Mexico, Albuquerque, New 87131 (e-mail address manelson@unm.edu) regarding clone availability
Seq primer: M13 Universal Forward Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry University of Oklahoma Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Other_ESTs: b3g07np.r1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: broe@ou.edu
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405 325 7762
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/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript" 3 146 c 123 g 97 t
                                                                                                      tissue_type="perithecia (fruiting/dev_stage="sexual"/lab_host="E. coli strain SOLR"
                                                                                                                                                                                         vector system"
                                                                                                                                                                                                                                                                    organism="Neurospora crassa"
/strain="wild type"
/db_xref="taxon:5141"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:5141"
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/lab_host="E. coli strain SOLR"
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                                                                                                                                                                                                                                              clone="b3g07np"
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46.5%;

Score 28.8;

DB 12;

Length 548;

Sordariomycetes;

mRNA sequence.

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REFERENCE
AUTHORS
                                          RESULT 5
BG280606
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                                                                                                                                                                                                                        Local
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                                                                                                                      ACACGGGCAGTGACAGAGAAAGAGAAATAAAGGAGACAGGTAAGGGGG 148
                                                                                                                                                 ATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGG 52
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 576)
  BG280606 585 bp mRNA linear c5b03np.fl Neurospora crassa sexual cDNA library,
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                                                                                                                                                                                                    36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biology University of New Mexico
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Fungal Genet. Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, B.,
Cushing, T., Errett, A., Fleharty, Gorman, M., Judson, K., Miller, R.,
Ortega, J., Pavlova, I., Perea, J., Todisco, S., Trujillo, R.,
Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Natvig, D.O./Nelson, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ngp@biology.unm.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet. Biol.
                                                                                                                                                                                                                                                                                              /note-"vector: pBlueScript SK (-); Site 1: EcoRI; Site 2: XhOI; mRNA isolated from 5 day old perithecia (fruiting bodies) of the fluffy strain fl a (Mating type a), fertilized with conidia from 74-OR23-IV A (Mating type A). cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XX vector system (Stratagene, La Jolla CA). Previously identified highly expressed clones were subtracted from this library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Fruiting Body"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Subtracted Perithecial"
/sex="Mating type a (fluffy), fertilized"
/tissue_type="Perithecia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5141"
/clone="SP6F6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Neurospora crassa"
/strain="fl a (FGSC 4347)"
                                                                                                                                                                                                                    46.5%;
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                                                                                                                                                                                                  Score 28.8; DB 9;
Pred. No. 1.2e+02;
D; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.26
); Mismatches
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    Uni-zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 08-FEB-1999
cDNA clone SP6F6
                        EST 21-FEB-2001
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AUTHORS
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ORGANISM
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DEFINITION
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AZ484766/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACACGGGCAGTGACAGAGAAAGAGAAATAAAGGAGACAGGTAAGGGGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESTS from a Neurospora crassa Sexual CDNA Library Unpublished (2001)
Other ESTs: c5b03np.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklaho
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 585)
Kupfer, D., Lai, H., Nelson, M. and Roe, B.
Kupfer, D., Lai, H., Nelson, M. and Roe, B.
Unpublished (2000)
Contact: Robert B.
University of Utah
                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
1 (bases 1 to 214)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reil
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,
                                                                                                                                                                                                                                                                                                                                   AZ484766 214 bp DNA li
1M0311P23F Mouse 10kb plasmid UUGCIM library
clone UUGCIM0311P23 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact Dr. Mary Anne Nelson, Department of
New Mexico, Albuquerque, NM 87131 (e-mail ac
regarding clone availability
Seq primer: M13 Universal Forward Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system Neurospora crassa
BG280606
                                                                           and Wright, D., Weiss, R.
Mouse whole genome sca
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                       Mus musculus
                                                             plasmid inserts
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                                                                                                                                                                                                                                                                                                                      AZ484766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Neurospora c
/strain="wild type"
/db_xref="taxon:5141"
/clone="c5b03np"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript; 3' end of cDNA cloned into XhoI site of pBlueScript" 161 c 126 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="perithecia (fruiting
/dev_stage="sexual"
/lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Neurospora crassa sexual cDNA library, Uni-zap/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:13079182
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    Genome Center
                        Weiss
                                                                               scaffolding with paired
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Pred. No. 1.2e+02;
0; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Biology, University of address manelson@unm.edu)
                                                                                   end reads
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Mus musculus genomic

52

585; 0

Gaps

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Pedersen, T., Reilly

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MEDLINE
COMMENT
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AQ165808/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 383)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                                AQ165808 383 bp DNA linear GSS 16-OCT-19: HS_3071_A1_G12_MR CIT Approved Human Genomic Sperm Library D Homo Bapiens genomic clone Plate=3071 Col=23 Row=M, DNA sequence.

AQ165808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddurn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0311 row: P column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                        Keller, A., Shaker, R.,
                                                                                                                                                                                                                                                                                                                                                AQ165808.1 GI:3564003
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Fax: 801 585 7177
                                                 99380589
                                                                                              scanning the human
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Migh quality sequence stop: 214.
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Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                    Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:10090"
clone="UUGC1M0311P23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%;
71.2%;
                                                                                              genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 17;
Pred. No. 1.5e+02;
D; Mismatches 15
                                                                                                                                                           Furlong, J., Young, J.,
                       Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                        Swartzell,S.,
g,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ212331 418 bp DNA linear GSS 18-SEP-1998 HS 2240 A2 G10 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2240 Col=20 Row=M, DNA sequence.
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37; Conserv
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401 Queen Anne Avenue North,
Tel: (206) 616-3618
                                                                                                                                                                                                                                          Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                Plate: 2240 rov
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
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E-Coli DH10B"
98 c 86 g 105 t 2 others
                                 E-Coli DH10B"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                    /clone lib="CIT Approved Human Genomic Sperm
/sex="male"
                                                                                                       /db_xref="taxon:9606"
/clone="Plate=2240 Col=20 Row=M"
                                                                                                                                                                         Location/Qualifiers
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                                                 note="Organ: sperm; Vector: pBeloBAC11; BAC Clones
                                                                                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                         ATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG279968 407 bp mRNA linear EST 21-FEB-2001 b7h08np.fl Neurospora crassa sexual cDNA library, Uni-zap vector system Neurospora crassa cDNA clone b7h08np 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, Un
620 Parrington Oval, Norman, OK 73019, US
Tel: 405 325 4912
Fax: 405 325 7762
                                      BE728034.1
                                                                         BE728034
601561322F1 NIH_MGC_
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact Dr. Mary Anne Nelson, Department
New Mexico, Albuquerque, NM 87131 (e-mai
regarding clone availability
Seq primer: M13 Universal Forward Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kupfer,D., Lai,H., Nelson,M. and Roe,B.
ESTS from a Neurospora crassa Sexual cDNA Library
Unpublished (2001)
Other_ESTs: b7h08np.r1
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Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
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BG279968
BG279968.1 GI:13077915
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                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
Xhoi; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
1 110 c 85 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Neurospora crassa"
/strain="wild type"
/db_xref="taxon:5141"
                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="sexual",
lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="perithecia (fruiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rector system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Neurospora crassa sexual cDNA library,
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Pred. No. 3.2e+02;
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                                                                                          mRNA line
s cDNA clone
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IMAGE:3830932
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AZ570132.1
                                                                                                                                                                                                                             Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (IDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informatic found through the I.M.A.G.E. Consortium/LLNL at: image plate: LLCM505 row: 1 column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
                                                                                                                                        Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malaria parasite P. vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ570132
270PvG10 Pv MBN #30 Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium vivax
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                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 670.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NIH MCC_20"
/tlosue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: /note-rorgan: skin; Vector: pOTB7; Site 1: XhoI; Site 2: /note-rorgan: skin; Vector: potaning. Directionally Cloned into EcoRI/XhoI sites using the following 5; cloned into EcoRI/XhoI sites using the following 5; adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubni (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
79 a 142 c 189 g 160 t
/organism="Plasmodium vivax"
/strain="Salvador I (Collins,
497-598)"
                                                                                            Location/Qualifiers
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Pred. No. 3.9e+02;
0; Mismatches 18
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vivax genomic 3', 1
                        Σ
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PEATURES
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SOURCE
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AQ410127
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo Bapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 397)
1 (bases 1 to 397)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,X., Swartzell,S., Adams,M.D. a.
                                                             Seq primer: SP6
Class: BAC ends
                                                                                                                     Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (linfo@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 659 row: B column: 9
                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ410127
HS_5083_B1_A05_SP6E_RPCI-11 Human Male_BAC_Library
genomic_clone_Plate=659_Col=9_Row=B, DNA_sequence.
                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scanning the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ410127.1
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        quality sequence stop: 397 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%;
ilarity 68.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site 1: ECOR V; Host leukocytes were extracted from P. vivax Infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) per 10 ml blood. Then blood was passed over a column of acid washed 0.1 mm glass beads, then through a Plasmodipur filter, followed by passage through a column of pre-wet whatman CF11 powder (1:2 ratio volume of blood to CF11), and finally centrifuged through a 50% percoll density cushion. Purified DNA was digested with mung bean nuclease in the presence of 44% formanide at 500C as described (Vernick, K. D., Imbershi, R. B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blunt-ended using T4 DNA Polymerase and size fractionated over a Sepharose CL-2B column. Fractions in the size range 500bp-4kb were ligated into the Eco RV site of pBluescript SK(+), and E. coli XI-10 Gold transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ing the human genome
Natl. Acad. Sci. U.S.A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligation mixture."
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/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:4432111
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Pred. No. 5.1e+02;
0; Mismatches 17
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VERSION

COMMENT

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5 ATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTAAG 62

Matches

TITLE

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SOURCE
ORGANISM
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AQ620909/c
                                                                              ORIGIN
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ORIGIN
                                                                                               BASE COUNT
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                    Query Match
Best Local
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                          Bource
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                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ATAAGGTCGGTGATTGTGAAAGAGACATAGAGGACACATGTAAGGTGGAAAATGTAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                           Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2178 row: H column: 5
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ620909 453 bp DNA linear GSS 16-JUN-1999
HS_2178_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2178 Col=5 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                      High quality sequence stop: 453
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping
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1 (bases 1 to 453)
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                                                                                                                                                                                                                                                                                                                                                                                                            Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scanning the human genome
                    Similarity
                                                                                                 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                               /note="Organ:
E-Coli DH10B"
a 59 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 50 c 61 g 138 t
                                                                                                                                                                       /db_xref="taxon:9606"
/clone="Plate=2178 Co1=5 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                        1. .453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=659 Col=9 Row=B"
                                                                                                                                                         'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="male"
                  42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%;
0;
Score 26.6; DB 17
Pred. No. 5.1e+02;
0; Mismatches 20
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Pred. No. 4.8e+02
                                                                                                                                     sperm; Vector: pBeloBAC11; BAC
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                                      Length 453;
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064P12 of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 649)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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GSS; genome survey seq
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                     2 (bases 1 to 649)
Roest-Crollius,H.,
                                                                     Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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Vector: pBluescript II KS
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Williams,G. and Brenner,S.
   Bouneau, L., Billault, A.,
                                                     Unpublished
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Jaillon,O., Dasilva,C., Fizames,C., lt,A., Quetier,F., Saurin,W., Bernot,
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
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1 (bases 1 to 371)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating imottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 5 05-OCT-2000;
                                                                                                                                                                                                                                                                           60;
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Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating fromottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 3 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                synthetic construct.
synthetic construct
artificial sequences.
                                                                                                                   371 bp
Sequence 5 from Patent WO0058485.
AX036739
AX036739.1 GI:11226248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct.
synthetic construct
artificial sequences.
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llarity 100.0%;
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llarity 100.0%;
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/db xref="taxon:32630"
/note="promoter MPr1116"
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Pred. No. 2.2e-10;
Mismatches 0;
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AX036754
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AX036753
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                                                                                                                                                                                                                                                                                                                       60;
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Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 19 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
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                                  1 (bases 1 to 462)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 20 05-OCT-2000;
                                                                                                                                                                        Sequence 20 from Patent AX036754
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GRUBER VERONIQUE (FR)
           MERISTEM THERAPEUTICS ; GRUBER VERONIQUE (FR
                                                                                                                   synthetic construct.
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/db_xref="taxon:32630"
/note="promoter MPr1146"
Location/Qualifiers
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/note="promoter MPr1162"
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                                                                                   artificial sequences.

1 (bases 1 to 9285)

Gruber, V. and Comeau, D.

Synthetic vectors, transgenic plants containing
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AX036756
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60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric expression promoters originating mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 22 05-OCT-2000;
                                                   for obtaining them Patent: WO 0118192-A 52 15-MAR-2001; MERISTEM THERAPEUTICS (FR)
                                                                                                                                                                                 Sequence 52
AX093047
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                                                                                                                                    synthetic construct.
synthetic construct
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1 (bases 1 to 600)

Rance, I., Theisen, M. and Gruber, V.
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="pMRT1336"
                                           Location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter MPr1165"
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6330 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGG 6385
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACAACCTAGAGG 56
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                                                                                                                                                                                                                                                                                                                                                                                                               TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAAACCAACAACAACCTAGAGG 7424
                                                                                                                                 complete genome; protease; reverse transcriptase; ribonuclease Commelina yellow mottle virus. Commelina yellow mottle virus Viruses; Retroid viruses; Caulimoviridae; Badnavirus. 1 (bases 1 to 7489)
                                                    Submitted (02-MAY-1990) Olszewski N.E., University of Minnesota, Dept of Plant Biology, 220 Biological Sciences Center, 1445 Gortner Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                       Commelina yellow mottle virus X52938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber, V. and Comeau, D. Synthetic vectors, transgenic plants containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic construct.
Medberry, S.L., Lockhart, B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial sequences.
                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                     X52938.1 GI:59047
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for obtaining them Patent: WO 0118192-A 57 15-MAR-2001;
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                  (revised by [4])
2 (bases 1 to 7489)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pMRT1342 results from the replacement of the expression cassette ep35S-gus-polyA35S from pMRT1335 by the expression cassette L5-gus-polyA35S isolated from pMRT1336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="pMRT1336 results from the insertion into pMRT1196 of the promoter MPT1165 isolated from plasmid pMRT1322 as described in PCT patent application PCT/IB00/00370" a 2252 c 2506 g 2087 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 from Patent W00118192.
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/db_xref="taxon:32630"
/note="pMRT1342"
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Pred. No.
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  and Olszewski, N.E.
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2e-08;
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4. (bases 1 to 7489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-DEC-1990)
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Direct Submission
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Direct Submission
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Nucleic Acids Res. 18 (18), 5505-5513 (1990)
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/codon_scarc=1
/codon_scarc=1
/proteIn_id="CAA37110.1"
/db_xref="GI:59050"
/db_xref="GI:59050"
/db_xref="GI:59050"
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/db_xref="GI:59050"
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YSHRSEBRMVVVNGSQVDRSFIOESSFEVLSRTGIEFHIGVMLVRIQILHRKFAGTM
ALIVFRDTRWSDDRAVLAMEIDLSECNQIVYVTLPDIMTIKSFYRHIQICVMTKGYD
GWQEEDNLLITTGGLTGRLSNYTSNVGFAYDVKAMVEHLQSNGVKAIKGEKWDAKRFHNG
GWNIEPSKVVVPMQPTEMKAVSNYDGTTSLRFSNYAAASTSKPPQYNEKDEEINEDEQ
EINHSLNLIINDEESTDEDERYQYQRYAMSQVGDSTFYDDTGWEEIDCRCNDLDEY
VPSETSTPTIDESEAIIDEFLEHAVEGRCDSDESLGGGDPRKYEYPTPQSFBEHLDNE
SRSRSSSASSTSMQDDVEEIVRLMKEMRMKKQKKKKAQQALSSQAQEEPIIEENIEEN
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ORAVNPAISGYSNYTAPTIKKVDRILRVFKKFN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /proteIn_id="CAA37108.1"
/db_xref="GI:59048"
/db_xref="SWISS-PROT:P19200"
/db_xref="SWISS-PROT:P19200"
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kklseevivetpevkinlrdlahnihiiahrvalgekviylylvdiifpllkniokso
                                                                                                                                                                                                                                                                                                                                                                                                            /note="3bp deletion in pCoYMV100"
1506. .7166
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/citation=[1]
                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                           note="ORF 3, 216 kD protein"
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REFERENCE AUTHORS TITLE

Rance,I., Theisen,M. and Gruber,V. Chimeric expression promoters originating mottle virus and cassava vein mosaic virus

from

commelina

ORGANISM

synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 243)

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AX036735.1

GI:11226244

243 bp Sequence 1 from Patent WO0058485. AXO36735

DNA

linear

PAT 16-NOV-2000

RESULT 10 AX036735 LOCUS

S

Matches

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7318

BASE COUNT ORIGIN

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Query Match
Best Local
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                                           1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGAGGATCC 60
TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACAACAACAAGAATAC 7377
                                                                                           54;
                                                                                                                   Similarity
                                                                                                                                                                                                            2662
                                                                                           Conservative
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PNFPGPAEVQMGVLKPKSGWRRPIQATLEEINCHHNWFAISTGGLACRSCKQFLAGVO
CHHCHAVYCFMCAEAYHDVQAEKIISKDYSFSARGKKGKAVIIEDEIGEFFLISQLO
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QENQRLQKQVERLQESLIMKLHREKDBALKHSEKASRVFSTIQESDBAELNLIKEELRQ
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GRILIGEGYFRMPVTYVMNMGLSPGIONIIGCSFIRSLEGGLRIEKDIIFFKLVTSI
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RSKIYSKFDLKSGFMQVAMEEESVPMTAFLAGNKLYEMLVMPFGLKNAPAIFQRKMON
VFKGTEKFIAVYIDDILVFSSTAEQBISQHLYTMLQLCKENGLILSPTKMKIGTPEIDF
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WRWRFKDEYQNLAKIANQDGGTQAILSQIRRIFLGEDPVLGQNTVQNIAFRKLKQLVC
PNYQSIRRYLMDYLTLAAETGLMWSETEGPAISEELFTKMPAAIGERVAQAYKIMDPT
                                                                                                                                                                                                       /note="g in clone pCoYMV100"
1389 c 1577 g 1861 t
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CEAIIKFYNKTNENKPSRVRWLTFSDFLTGLGITVTFEHIDGKHNGLADALSRMINFI
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RQKMAPTGDKRMNPETWKMVRQIKEKVKNLPDLQLPPKDSFIIIETDGCMTGWGAVCK
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                                                                                                                                                                                                                                                                                /note="c in
                                                                                                                                                                                                                                                                                                                         note="additional t in pCoYMV100"
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                                                                                                              Score 50.4; DB 14; Pred. No. 1.5e-06;
                                                                                           Mismatches
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                                                                                                                                  Length
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                                                                                         Gaps
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promoter
BASE COUNT
ORIGIN
                                                  REFERENCE
AUTHORS
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AX036755
LOCUS
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KEYWORDS
                                                                                                                                                                     RESULT 12
AX036741
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Best Local Similarity
Matches 49; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                   195 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAAC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct.

M synthetic construct

A strificial sequences.

1 (bases 1 to 392)

1 (bases 1 to 392)

Rance, I., Theisen, M. and Gruber, V.

Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus

Patent: WO 0058485-A 21 05-OCT-2000;

WERISTEM THERAPEUTICS (FR); RANCE IANN (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAAC 49
                                                         synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 301)
                                                                                                                               301 bp
Sequence 7 from Patent WO0058485.
AX036741
 Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 7 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
                                                                                                                        AX036741.1
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AX036755
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MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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                                                                                                                                                                                                                                                                 77.8%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1164"
1. . 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="243 bp promoter fragment from
of Commelina Yellow Mottle Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
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53 c
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Pred. No.
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; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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thes 0;
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AUTHORS
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KEYWORDS
SOURCE
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AX036738
LOCUS
DEFINITION
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DEFINITION
                                                                                                                                                                                                      RESULT 14
AX036740
                                                                                                                                   SOURCE
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Best Local S
Matches 46
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15 ACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGAGGATCC 60
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                                                                                                                                                                                                                                                                                                                                              ACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCC 348
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          artificial sequences.

1 (bases 1 to 398)

Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 6 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                       Sequence 6 from AX036740
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Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 4 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
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46; Conserv
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AX036738
                                                                                                                                                                     synthetic construct.
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/db xref="taxon:32630"
/note="promoter MPr1117"
1. .348
1. .348
1. .70 c 78 g 84 t
Location/Qualifiers
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/note="promoter MPr1154"
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100.0%; Pr
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54 c
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Patent WO0058485.
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0; Mismatches
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Pred. No. 6.9e-05;
0; Mismatches 0;
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7.1e-05;
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                                   THEISEN
                                                                                   commelina yellow
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                                   MANFRED (FR)
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promoter
BASE COUNT
ORIGIN
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
AX036759
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Search completed: May 11, 2003, 06:04:58 Job time: 672.263 secs
                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                      Query Match
Best Local Similarity
Matches 46; Conserva
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                                                                                                                                                                                                                                                                                                                                  artificial sequences.

1 (bases 1 to 472)

Rance, I., Theisen, M. and Gruber, V.

Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus

Patent: WO 0058485-A 25 05-007-2000;

MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); THEISEN MANFRED (FR);

GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX036759 472 bp
Sequence 25 from Patent WO0058485.
AX036759
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                                                                                                                                      73.0%; Score 46; DB 6; Length 472; illarity 100.0%; Pred. No. 6.6e-05; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:32630"
/noTe="promoter MPr1169"
1.472
92 c 112 g 119 t
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80 c
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/db_xref="taxon:32630"
/note="promoter MPr1147"
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9	89	7	σ	U	4	w	N	_	Result
46	49	49	60	60	60	60	60	63	Score
73.0	77.8	77.8	95.2	95.2	95.2	95.2	95.2	100.0	Query Match
301	392	243	600	462	393	371	317	63	% Query Match Length DB
21	21	21	21	21	21	21	21	21	DB
AAA96841	AAA96855	AAA96835	AAA96856	AAA96854	AAA96853	AAA96839	AAA96837	AAA96846	ID
Nucleotide sequenc	Nucleotide sequenc	Promoter from inte	Nucleotide sequenc	Directional desoxy	Description				

4 4 5 4	C 43	42	c 41	40			c 37		35	c 34	33	32	31	c 30	29	28	27	26	25	24	23	22	21	c 20		18	17	16	15	14	13	12	11	10
23.2	23.4	23.4	23.6	•	23.6	•	23.8	•	•	24	24	24	24	24	24	24.4	.4	٠.	24.4	4.	4	24.8	24.8	25	25.8	26	26.4	27	27	46	46	46	. 46	46
36.8	37.1			•		•	•	•	•					•	٠	38.7	38.7	38.7	38.7	38.7	39.0	39.4	39.4	39.7	41.0	41.3	41.9	42.9	42.9	73.0	73.0	73.0	73.0	73.0
411	14872	6847	5102	2462	1203	19603	10369	10369	10202	3245	1034	1032	1023	777	329	53075	52562	2915	2418	2203	1196	1969	815	694	14919	4289	2786	4600	2928	604	541	472	398	348
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ABV46444	AAV52205	ABL14139	ABL92274	ABL22798	AAS80397	ABL02570	ABL32393	AAS46304	ABL02571	AAH54626	AAX27315	AAX27434	AAH33092	ABN66600	AAI87625	AAK86671	AAK86669	AAS21348	AAI58281	AA160067	ABL40669	AAH14864	AAF15867	AAF14716	AAS46505	ABL03686	AAH14506 ·	AAS68229	AAS89944	AAA96857	AAA96858	AAA96859	AAA96840	AAA96838
Human prostate exp	Streptococcus pneu	Drosophila melanog		Drosophila melanog	DNA encoding novel	Drosophila melanog	Human immune syste	Tumour suppressor	Drosophila melanog	S. epidermidis gen	Human secreted pro		Human colon cancer	Streptococcus poly	Human polynucleoti	Human immune/haema	Human immune/haema	Human cDNA sequenc	Human polynucleoti		Human Fe-S protein	Human cDNA sequenc	Human prostate can	Aspergillus oryzae	Tumour suppressor	Drosophila melanog	Human cDNA sequenc	DNA encoding novel	DNA encoding novel	Nucleotide sequenc			Nucleotide sequenc	Nucleotide sequenc

ALIGNMENTS

RESULT 1 AAA96846

AAA96846 standard; DNA; 63 ₽₽

AAA96846;

19-FEB-2001 (first entry)

Directional desoxynucleotide building block S5

Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; ss.

Synthetic.

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370

29-MAR-1999; 99FR-0003925.

Rance I, Gruber V, Theisen M;

(MERI-) MERISTEM THERAPEUTICS.

WPI; 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises

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RESULT 2
AAA96837
ID AAA9
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Best Local
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                                                                            Chimeric sequence
                                                               with
                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a directional desoxynucleotide building block, which was used to construct chimeric promoters of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are
                    Claim
                                                                                                                           WPI; 2000-647238/62.
                                                                                                                                                       Rance I,
                                                                                                                                                                                                                29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                             plant green
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                                                                                                                                                                                    (MERI-) MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                 transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                           Promoter; intergenic region; Commelina yellow mottle virus;
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                                                         eric expression promoter for transgenic plant production, comprises ence from promoter comprising vascular expression region replaced sequence from promoter comprising green tissue expression region
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                    <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                  Page
                                                                                                                                                                                                                                                                                                                                                                              expression promoter; plant vascular expression promoter; sen tissue expression promoter; Cassava vein mosaic virus ic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                     Gruber V,
                                                                                                                                                                                                                                                                                                                                    Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of chimeric expression promoter MPr1116
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                    81;
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       The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mossic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
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plant gre
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                                                                                                                                                                                                                                                  Chimeric expression promoter for transgenic plant production, of sequence from promoter comprising vascular expression region rewith sequence from promoter comprising green tissue expression
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Chimeric -
                                                                                                                                                   The present sequence represents a chimeric promoter of the invention 
The specification describes chimeric expression promoters. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression pro
                                                                                                                                                                                                    Claim 5;
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                                                                                                                                                                                                    Page 81; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                       Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Commelina yellow
Cassava vein mosa
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Best Local :
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                                                                                                           The present sequence represents a collective promoters. These chimeric specification describes chimeric expression promoters to derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                          Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus;
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                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                               Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2000; 2000WO-IB00370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plant; chimera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of chimeric expression promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA96853 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGAGGATCC 60
             TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
                                             60;
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                        MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                       Page
                                                                                          393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 BP; 122
                                                                                                                                                                                                                                                                                                                                                               Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Commelina yellow mottle virus.
                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                              99FR-0003925.
                                                                                          128
                                                                                                                                                                                                                                                         91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%;
                                                                                         Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α.
                                                        95.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                               Theisen M;
                                                                                         75 C; 93 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 C; 89 G;
                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                          Score 60; DB; Pred. No. 1.1
                                          ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
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                                                                                          97
                                                                                         Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멂
                                                        1.1e-11;
                                                                 DB 21; Length 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-11;
                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                         other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                             Indels
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                                          Gaps
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RESULT 6
AAA96856
ID AAA9
XX
AC AAA9
AC AAA9
XX
DT 19-F
XX
DE Nucl
                                                                                                                                                                                                  Matches
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Best Local (
                                                                                                                                                                                                                                                                               The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric expression promoter for transgenic plant production, esequence from promoter comprising vascular expression region rewith sequence from promoter comprising green tissue expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric expression promoter; plant vascular expression plant green tissue expression
                                                                                                                                                                                                                                                Sequence 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96854 standard; DNA; 462
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a chimeric promoter of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-647238/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96854;
                                     19-FEB-2001
                                                                                     AAA96856 standard; DNA; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI-)
                                                                                                                                                403
                                                                                                                                                                        1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGAGGATCC
                                                                                                                                                                                                                                                                         producing transgenic plants.
                                                                                                                                                5.
                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MERISTEM THERAPEUTICS
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          Page 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                BP; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-IB00370
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                          91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimera;
                                                                                                                                                                                           95.2%; but
100.0%; Pr
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Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                A; 87 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric expression
                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                               Score 60; DB:
; Pred. No. 1.20
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                     ВP
                                                                                                                                                                                                                                                111 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter;
                                                                                                                                                                                                            1.2e-11;
                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                        Length
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                  0,
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                                                                                                                                                  462
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Nucleotide sequence of chimeric expression

promoter MPr1165

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic soid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                  Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus;
                                                                                     Commelina yellow
                                                                                                                      plant green tissue expression transgenic plant; ss.
                                                                                                                                                                                                        Promoter
                                                                                                                                                                                                                                       19-FEB-2001
                                                                                                                                                                                                                                                                                                        AAA96835 standard; DNA; 243 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2000; 2000WO-IB00370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Commelina yellow mottle vi
Chimeric - Cassava vein mosaic virus.
                       05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 86-87; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-647238/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic plant; chimera;
                                                      WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                        541
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                                                                                                                                                                                                                                                                                                                                                                                                                       μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      producing
                                                                                                                                                                                                                                                                                                                                                                                        TTCCTTATTTAAGCACTTGTAGTAGCTTAGAAAACCAACACAACAACCTAGAGGATCC 600
                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACACAACAACCTAGAGGATCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERISTEM THERAPEUTICS.
                                                                                                                                                                                                      from intergenic region of Commelina yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Commelina yellow mottle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 A; 111 C; 147 G; 154 T; 0 other;
                                                                                       mottle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 21; Pred. No. 1.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 600
                                                                                                                                                                                                      mottle virus
                                                                                                                                       virus;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a promoter fragment from the intergenic region of Commelina yellow mottle virus. The promoter is a strong promoter in vascular and reproductive tissues. The promoter is used to construct chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. The chimeric promoters are useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric expression promoter for transgenic plant production, c sequence from promoter comprising vascular expression region re with sequence from promoter comprising green tissue expression
                                     Rance I,
                                                                                                                                                  05-OCT-2000
                                                                                                                                                                                                       Chimeric -
Chimeric -
                                                                                                                                                                                                                                                          chimeric expression promoter; plant vascular expression plant green tissue expression promoter; Cassava vein mos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 243 BP; 71 A; 53 C; 45 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-647238/62
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           WPI; 2000-647238/62
                                                                                           29-MAR-1999;
                                                                                                                     29-MAR-2000;
                                                                                                                                                                             WO200058485-A1
                                                                                                                                                                                                                                               transgenic plant; chimera; ss
                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of chimeric expression promoter MPr1164
                                                                                                                                                                                                                                                                                                                                             19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                       AAA96855;
                                                                                                                                                                                                                                                                                                                                                                                                   AAA96855 standard; DNA; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 79; 91pp; English.
                                                                 (MERI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                 MERISTEM THERAPEUTICS
                                     Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gruber V,
                                                                                                                                                                                                                                                                                       intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                     Commelina yellow mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                      2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99FR-0003925
                                                                                           99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                     Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; I
7.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                             mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                            virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant green tissue expression (Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.
                                                                                                                            Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region.
The present sequence represents a chimeric promoter of the invention The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression
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                                                                                                                                                                                                                                                                   (MERI-) MERISTEM THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoters comprise a nucleic acid sequence which is deri-
irst plant promoter, in which a plant vascular expression
                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 86;
                                                                                                                                                                                                                                 Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Commelina
Cassava ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                                                   2000WO-IB00370
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                                                                                                                                                                                                                                                                                                    99FR-0003925.
                                                                               91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes chimeric expression promoters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    llow mottle virus.
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Query Match

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RESULT 10
AAA96838
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Best L
The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
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Chimeric -
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                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                  sequence from with sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999;
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transgenic plant; chimera; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of chimeric expression promoter MPr1117
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                                                                                                                                                                                                                                                                           5; Page 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commelina yellow mottle virus.
Cassava vein mosaic virus.
                                                                                                                                                                                                sequence represents a chimeric promoter of the invention cation describes chimeric expression promoters. These
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                                                                                                                                                                                                                                                                                                                                             promoter comprising vascular expression region replaced from promoter comprising green tissue expression region
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RESULT 12
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                                                                                                              Query Match
Best Local
                                                                                                     Matches
                                                                                                                                                                              The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant green tissue expression commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
  AAA96859 standard; DNA; 472 BP
                                                                                                                                                                                                                                                                                                                                      Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
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Chimeric -
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                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI-) MERISTEM THERAPEUTICS.
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                                                                                                                                                                      transgenic plants.
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                                                                                               73.0%; but
100.0%; Pr
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9.7e-07;
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                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                Query Match
 Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic transgenic plant; chimera; 88.
                                                        Nucleotide
                                                                                                                          AAA96858 standard; DNA; 541
                                                                                                                                                                                                                                                                        Sequence 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000
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                                                                               19-FEB-2001
                                                                                                    AAA96858
                                                                                                                                                                                 427
                                                                                                                                                                                                     15
                                                                                                                                                                                                                                       Local
                                                                                                                                                                               ACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCC 472
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(first

entry) of chimeric

expression

promoter

ion promoter; mosaic virus

ВP

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The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Perferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Commelina yel
Chimeric - Cassava vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression proplant green tissue expression promoter; Cassava vein mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 88; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; chimera; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of chimeric expression promoter MPr1169
                                                                                                                                                                                                                         producing
ACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGAGGATCC 60
                                                       46;
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                         from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Commelina yellow mottle virus
                                                       Conservative
                                                                                                                                                                 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
                                                                                                                                                                                                                                                   intergenic regions. The chimeric promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                         transgenic plants.
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                                                                                     100.0%;
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                                                                                                               73.0%;
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                                                       0,
                                                                                  Score 46;
Pred. No.
                                                          Mismatches
                                                                                                               BB
                                                                                     1e-06;
                                                                                                               21;
                                                          0
                                                                                                         Length 472;
                                                       Indels
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                                                                                                                                                                                                                                                         are useful
                                                       0,
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RESULT 14
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                 chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                    Nucleotide sequence of chimeric expression promoter MPr1167
                                                                                                                                                                                                                                                    19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 541 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647238/62
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Chimeric -
29-MAR-1999;
                          29-MAR-2000; 2000WO-IB00370.
                                                     05-OCT-2000
                                                                                 WO200058485-A1
                                                                                                                                                                                             Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                496
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                                                                                                                                                                                                                                                                                                                                                                                                        15 ACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification describes chimeric expression promoters.
                                                                                                                                                                                                                                                                                                                                                                             ACTTGTGTAGTAGCTTAGAAAAACCAACACAACCAACCTAGAGGATCC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 87-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Commelina yellow mottle virus. Cassava vein mosaic virus.
                                                                                                          Commelina yellow mottle yirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic
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99FR-0003925
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Query Match
                                                                                                                    a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                       The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                            Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 87; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI-) MERISTEM THERAPEUTICS
                                                                                                   producing transgenic plants.
                                                                                                                                                                                                                                                                                                              present sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theisen M;
Score 46;
Pred. No.
DB 21;
1e-06;
                   21;
                 Length 604
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RESULT 15
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Matches
                                                                                                                                                      AAS89944 standard; cDNA; 2928
                                                                                                                                    13-FEB-2002
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Local

Similarity

0

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

forensic;

DNA encoding novel human diagnostic protein #25748

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

WPI; 2001-639362/73. P-PSDB; ABG25757.

Drmanac

RT,

Liu C,

Tang

(HYSE-) HYSEQ INC.

31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

30-MAR-2001; 2001WO-US08631

11-OCT-2001 WO200175067-A2 Homo sapiens

Claim 1; SEQ ID No 25748; 103pp; English.

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CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC cand gene mapping, and in recombinant production of (II). The CC cand gene mapping, and in recombinant production of (II). The CC cand gene mapping, and in recombinant production of (II). The converse converse
                                                                                                                                                                 Sequence 2928 BP; 742 A; 773 C; 737 G; 676 T; 0 other;
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Gaps
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Search completed: May 11, 2003, 03:04:03 Job time : 124.526 secs 밁 Query Match 42.9%; Score 27; DB 23; Length 2928; Best Local Similarity 85.7%; Pred. No. 7; Matches 30; Conservative 0; Mismatches 5; Indels 903 CTTCGCTAGCCAACACAACAGCCTAGAGGATCCCC 937 28 CTTAGAAAACCAACAACAACCTAGAGGATCCCC 62

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Result
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Maximum Match 100%
Listing first 45 summaries
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        Score

    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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63
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-911-434A-5

US-08-920-812-4

US-08-920-812-4

US-08-920-817-4

US-08-920-827-4

US-08-920-828-4

US-08-920-828-4

US-08-920-828-4

US-08-755-587-4

US-08-755-587-1

US-08-755-587-1

US-08-755-587-1

US-08-755-587-1

US-08-755-587-1

US-08-966-106-3

US-08-966-106-3

US-08-968-106-3

US-08-968-106-3

US-08-968-106-3

US-08-968-106-3

US-08-968-106-3

US-08-968-106-3

US-08-968-106-3

US-09-9453-7028-266

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18	18	0/055,7	0/055,722	8	0/051,928	080,051,91	8	/052,7	0/052,73	8	0/051	0	08	08 0/051	0/051,91	0/051,932	08	08	0/052,732	60/052,803	0	08 0/051.929	0/051,925	0/052,79	8	0/051,92	T/US98 7	8	S/09/227	Secrete			ion US/09227357		ALIC	-80-	6	-08-4	-09-1	09-7	-09-0	9 6	-80	09-	-80-	-09-	-09-	-09-
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EARLIER FILING DATE: 1997-08-18

APPLICATION NUMBER: 60/055,949

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US-09-227-357-15
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Best Local
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LENGTH: 1032
                                                                                                                                                                                                                                                                           Sequence 15, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
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EARLIER
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SOFTWARE: Patentin Ver. 2.0
EQ ID NO ''''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: n eq
                                                    EARLIER
EARLIER
                                                                                                                                                                                   FILE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
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TITLE OF INVENTION: 123 Human Secreted Proteins
                                                                                                                      EARLIER
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                                                                                                                                                                       EARLIER APPLICATION NUMBER: PCT/US98/13684
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LOCATION: (593)
OTHER INFORMATION: n
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APPLICATION NUMBER: 60/052,793
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,925
FILING DATE: 1997-07-08
                                                                                                                                   FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/051,926
APPLICATION NUMBER: 60/051,929
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,803
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APPLICATION NUMBER: 60/058,661
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,660
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APPLICATION NUMBER: 60/055,684
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APPLICATION NUMBER: 60/056,360
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APPLICATION NUMBER: 60/055,964
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FILING DATE: 1997-09-12
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RESULT 3 US-08-961-527-72/c

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Gaps

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; SOPTWARE: PatentIn Ver. 2; SEQ ID NO 15; LENGTH: 1034; TYPE: DNA; ORGANISM: Homo sapiens US-09-227-357-15
                                          Query Match
Best Local Similarity 68.8
Conservative
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1 TTCCTTATTTAAGCACTTGTGTAGTAGCTAGAAAACCAACACACAA 48
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APPLICATION NUMBER: 60/051,931
FILING DATE: 1997-07-08
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ILING DATE: 1997-08-18
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LING DATE: 1997-08-18
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                                                     Score 24; DB Pred. No. 8; 0; Mismatches
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Sequence 72, Application US/08961527 Patent No. 6420135

ENERAL INFORMATION:

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                                                                   ; OTHER INFORMATION: ubiquitin carboxyl-terminal hydrolases family
US-09-280-116-245
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                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 518
                                                                                                                                                                                                                                                       Sequence 245, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
PILE REFERENCE: 5800-24, 035800/176965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                     TYPE: DNA
                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1596 TCCCTGCATTAAACAATAGATAAGTACCAAAGATAACCAGCAAAACAGCTAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HP Vectra
OPERATING SYSTEM: MS
SOPTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double
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                35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PB340P1
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Pred. No. 22;
0; Mismatches
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              Score 22.4;
Pred. No. 2
 Mismatches
                                DB 4; Length 518;
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US-08-911-434A-5/c
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                                                                                                                                                             RESULT 6
                                                                                                                                              US-08-920-812-4
                                                                                                                                                                                                                                                                                                                                             US-08-911-434A-5
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                                                                                                          Sequence 4, Application US/08920812
Patent No. 5763188
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TORIKA
APPLICANT: OEDA,
                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
NUMBER OF SEQUENCES:
                  FITLE OF
                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313. ATTTAATCAGGCATTGGGAAGACCAGAAAAAATTCACAACAAATTAGAATTTCCCCC 368
                                                                                                                                                                                                             724 AAGCACTTATATTGAAGCTTAAAAGCCCCCAAAAAAAGAAGTTAG
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                           11 AAGCACTTGTGTAGTAGCTTAGAAAACCAACACCAACAACCTAG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 12-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Daucus carota L. INDIVIDUAL ISOLATE: Kuroda
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Raymer REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                          h 35.2%;
Similarity 69.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
               INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        836 base pairs
                                                         Matsuhisa,
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703) 205-8050
                                             Uehara, Hirotsugu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         terminator
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                                                                             Tsuneya
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               Probe for Diagnosing Infectious Disease
25
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                                                                Akio
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Pred. No. 33;
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                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                           13;
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CORRESPONDENCE ADDRESS:

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Best Local Similarity 63.0%;
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pair
                                                                                                                                                                                 NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
ADDRESSEE: Marshall Tower, 233
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1639
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APPLICATION NUMBER: US 0:
FILING DATE: 27-MAR-1995
                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      APPLICANT: Eda, SO TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                     APPLICANT: Matsuhisa, Akio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus aureus STRAIN: Clinical Isolate SA-77
   APPLICATION
                                                                                                                                                                   CITY: Chicago
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                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCTGAATGAAGCATTTTATTTTTAAATATGATAGCCAATATAACAAGCTATA 1692
                                                                                                                    RY: United States of America 60606-6402
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                                                                                                                                                     Illinois
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: United States of America
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                                                                                                                                                                                                                                                                                    Uehara, Hirotsugu
                                                                                                                                                                                                                                                                                                                       Ohno,
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   NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                   Teuneya
                                                                                                                                                                                                                                                   Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/362,577
US/08/920,827
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Pred. No. 50;
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South Wacker Drive
                                                                                                                                                                                      South Wacker Drive
                                                                                                                                                                                                    Gerstein, Murray & Borun
                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 2885;
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RESULT 8
US-08-921-177-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 33,547
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION - 710,7710
                                                                                                                                  APPLICATION NUMBER: US 08/362,577 FILING DATE: 27-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ADDITION: TO COLOR
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Re-
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: (
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 27-MAR-
                                                               REGISTRATION NUMBER: 33,54:
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
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                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRAIN: Clinical Isolate SA-77
                                 TELEFAX:
                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACACAACAACCTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rin-Laures, Li-Heien REGISTRATION NUMBER: 33,54
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 2885 base pairs
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                                                                                                                                                                                                                                                                                                                                                            60606-6402
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Similarity 63.0%;
                                                                                                                                                                                                                                                                                                                                                                                            Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                    Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
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                                 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                            United States of America
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                                                                                                                                                                                                                                                                           PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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00 Sears Tower, 233 South Wacker Drive
                                                   312/474-6300
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                                                                                                   33,547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22;
Pred. No.
                                                                                    19036/32420
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                                                                                                                                                                                                                                                                           Version #1.25
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SEQUENCE CHARACTERISTICS:

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                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1639 TTGCTGAATGAAGCATTTTATTTTTAAATATGATAGCCAATATAACAAGCTATA 1692
                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pair
                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: Patentin Residence APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: (
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                             Local
                                                                                                                  ORGANISM: Staphylococcus STRAIN: Clinical Isolate
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27
CLASSIFICATION:
                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus aureus STRAIN: Clinical Isolate SA-77
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                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       NAME: Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGA 54
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Similarity
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                                                                                                                                                                                                                                                                                312/474-0448
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uehara, Hirotsugu
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                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                               312/474-6300
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00 Sears Tower, 233 South Wacker Drive
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63.0%;
                                                          34.9%;
63.0%;
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                                                                                                                  aureus
SA-77
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                                                           Score 22; DB
Pred. No. 50;
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Pred. No. 50;
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                                             Mismatches
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                                                                         DB 1;
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RESULT 11
US-08-755-587-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
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                                                                                                                        sequence 4, Application US/08755587 Patent No. 6045997
                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                         GENERAL INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1097
                                                                                                                                                                                                                              1639 TTGCTGAATGAAGCATTTTATTTTTAAATATGATAGCCAATATAACAAGCTATA 1692
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
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                                                                        APPLICANT:
                     APPLICANT:
TITLE OF I
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
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     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                               1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACAACCTAGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus STRAIN: Clinical Isolate SA-77
                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                    Similarity
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                    I: Stratton, Michael R
INVENTION: Materials
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2885 base pairs
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Uehara, Hirotsugu
                                                 Ashworth, Alan
                                                                       Wooster,
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohno,
                                                                                       Futreal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                   Phillip A
Richard F
                                                                                                                                                                                                                                                                                                                  34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe for Diagnosing Infectious Disease
Materials and methods relating to the identification and sequencing of the BRCA2 cancer
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Pred. No. 50;
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 81
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         FITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                      PPLICANT: Futreal, F. PPLICANT: Wooster, R. PPLICANT: Ashworth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9: FILING DATE: 14-DEC-1995
                                                                                                                                                                     STREET:
                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 APPLICATION NUMBER:
                                                                                  EDIUM TYPE:
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              APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                               Application US/08755587
                                                                                                                                                                    E: Bell Seltzer Park & Gibson
310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 base pairs
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310 UCB Plaza,
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                                                                                                                     USA
                                                                                                                                                                                                                                                                                        Stratton, Michael R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                              PatentIn Release #1.0,
                                                                                  Floppy disk
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Plaza, 3605 Glenwood Avenue,
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                                                                                                                                                                                                                                                                                                                           Phillip A
Richard F
                                                                                                                                                                                                                                Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
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US/08/755,587
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Pred. No. 3
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                              Version #1.25 (EPO)
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                              APPLICATION NUMBER: GB 9523959.6 FILING DATE: 23-NOV-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                            FILING DATE: 25-NOV-
                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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                                                                                       GB 9525555.0
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GB 9617961.9
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Pred. No. 4
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PILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

31,665

Kenneth D Sibley

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Query Match
Best Local Similarity
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Patent No. 6261561
GENERAL INFORMATION:
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                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCKEE, MCKEE, Alison D.
O'Brien, Alison D.
Wachtel, Marian R.
Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That Express Int
Alone Or As A Fusion Protein With One Or More Other
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,466A
PILING DATE: 18-Apr-1997
CLASSIFICATION: <Unknown>
ATTORNEY AGENT INFORMATION:
                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                     NAME: BOONE, LAUIAI S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                         SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabo
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                   TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
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34.6%;
61.4%;
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Score 21.8;
Pred. No. 60;
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                  DB 4;
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                  Length 3131;
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Search completed: May 11, 2003, 03:07:40 Job time : 30.2632 secs
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GENERAL INFORMATION:
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                                                                                                                                                    Matches
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                                                                         47
                                                                                                                                                                    Local
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                                                                                                            1 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACACCAACAACCTAGAGGA 57
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/840,466
FILING DATE: 1997-04-18
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BOONE, LAURAI S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That
Alone Or As A Fusion Protein With One Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stewart, C. Neal
                                                                         TTTGGTATTACATAATCAGGGAATAACATTAGAAAACGAACATATGAAAATAGAGGA
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                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/696,188B FILING DATE: 26-Oct-2000 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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O'Brien, Alison D.
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Pred. No. 60;
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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63
          May 11, 2003, 03:08:16 ; Search time 62.3684 Seconds (without alignments) 1255.289 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                                                  US-09-963-803-12
US-09-963-803-3
US-09-963-803-5
US-09-963-803-19
US-09-963-803-22
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US-09-963-803-7
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US-09-963-803-24
US-09-963-803-23
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Sequence 12, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 25, Appli
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Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
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Match Local S: es 63 1 TTCC 1 TTCC 61 CCG 6	3-803-12 LL INFORMAT ROF INVENT ROF INVENT ROF INVENT ROF INFORMAT ROF SEQ INA	00000000000000000000000000000000000000
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RESULT 2 US-09-963-803-3 ; Sequence 3, Application US/09963803

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FITLE OF INVENTION.

PILE REPERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR APPLICATION NUMBER: PCT IB00/00370
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SEQ ID NO 9
LENGTH: 371
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NAME/KEY: promoter
LOCATION: (1)..(317)
THER INFORMATION:
JS-09-963-803-3
                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
Matches 60; Conservative
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR APPLICATION NUMBER: PCT IB00/00370
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: Date: 2000-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein monato virus
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                                                                                                                                                                                     NAME/KEY: promoter LOCATION: (1)..(371) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Promoter MPr1116
                                                                                                                                                                                                                                                                                OTHER INFORMATION: promoter MPr1146
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312
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                                                                                  Conservative
                                                                                                    95.2%; Score 60; DB 9; L
100.0%; Pred. No. 1.8e-12;
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; Pred. No. 1.7e-12;
                                                                                  Mismatches
                                                                                                                        Length 371
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RESULT 5
US-09-963-803-20
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       Matches
                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
DBTIOR BODITON NUMBER: FOR TOWN NOT THE PRIOR TOWN NUMBER: PR
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: FCT IB00/00370
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT IB00/00370 PRIOR FILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39
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TITLE OF INVENTION: Chimeric expression promoters originating
TITLE OF INVENTION: virus and cassava vein mosaic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
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OTHER INFORMATION:
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                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                           NAME/KEY: promoter LOCATION: (1)..(46)
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                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                      Local
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No. US20030028922A1
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   95.2%; Scilarity 100.0%; For Conservative 0;
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100.0%; Pr/
0;
                                      Score 60; DB 9; L; Pred. No. 1.9e-12;
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Pred. No.
       Mismatches
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. 1.8e-12;
0; Indels
                                                                            Length 462
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                                                                                                                                                                                                                                                  LENGTH: 243
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SEQ ID NO 22
LENGTH: 600
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Best Local Similarity
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Publication No. US20030028922A1
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/963;803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT IB00/00370 PRIOR FILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 39
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
                                                                                   NAME/KEY: promoter LOCATION: (1)..(243) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: promoter LOCATION: (1)..(600) OTHER INFORMATION:
                                                                                                                                                                 OTHER INFORMATION: 243 bp Fragment from the intergenic region of commelina yellow OTHER INFORMATION: ttle virus
                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus and cassava vein mosaic virus
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100.0%; Pred. No.
77.8%;
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Score 49;
Pred. No.
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DB 9; L
. 1.7e-08;
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US-09-963-803-7
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Publication No. US20030028922A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow |
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
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CURRENT FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 39
NAME/KEY: promoter LOCATION: (1)..(301) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
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                                                                                                                           LENGTH: 301
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                       FEATURE:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 TTCCTTATTTAAGCACTTGTGTAGTAGCTTAGAAAAACCAACAACAAC
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US-09-963-803-6
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                                                                                                                                                                                                                                                                             Sequence 6, Application US/09963803
Publication No. US20030028922A1
GEMERAL INFORMATION:
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: VITUS and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT FILING DATE: US/09/963,803
CURRENT FILING DATE: 0001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR REPLICATION NUMBER: DESCRIPTION PRIOR FILING DATE: 1999-03-29
PRIOR REPLICATION NUMBER: DESCRIPTION PRIOR FILING DATE: 1999-03-29
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SEQ ID NO 4
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09963803 Publication No. US20030028922A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR APPLICATION NUMBER: DCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEO ID NOS: 39
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT IB00/00370 PRIOR FILING DATE: 2000-10-05 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                SOFTWARE: PatentIn version 3.1
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                                              FEATURE:
OTHER INFORMATION: promoter MPr1147
                                                                                        LENGTH: 398
TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: promoter MPr1117
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NAME/KEY: promoter
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Local Similarity 100.0%; Pred. No. 2.3e-07
es 46; Conservative 0; Mismatches 0
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100.0%; Pred. No. 2.2e-07;
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US-09-963-803-25
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                                                                                                SEQ ID NO 24
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APPLICANT: Meristem Therapuetics
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Publication No. US20030028922A1
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APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating
TITLE OF INVENTION: virus and cassava vein mosaic virus
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: FCT IB00/00370
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                              FILE REFERENCE: 184333042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
CURRENT PLING DATE: FR 99/03925
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
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                                                                                                                    SOFTWARE:
                                                                                                                                            NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: promoter LOCATION: (1)..(472) OTHER INFORMATION:
                                                 TYPE: DNA
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OTHER INFORMATION: promoter MPr1169
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TYPE: DNA
    FEATURE:
                        ORGANISM: Artificial Sequence
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                                                                     ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 ACTIGIGIAGIAGCITAGAAAACCAACAACAACCTAGAGGATCC 472
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Local Similarity 100.0%;
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                                                                                                                      PatentIn version 3.1
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2.4e-07;
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Best Local S
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Best Local Similarity
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                                                                               APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jame
APPLICANT: Mannion, Jame
APPLICANT: MANNION, COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEWATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR PILING DATE: 2000-03-01
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
               PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: promoter MPr1167
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            559 ACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCC 604
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FILING DATE: 2000-04-27
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100.0%; Pred. No. 2.7e-07;
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                                                                                                                                                 ; OTHER INFORMATION: n=A,T,C or G US-09-796-692-6196
                                                                       Best Loc
Matches
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LENGTH: 373
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                    FEATURE:
NAME/KEY: unsure
LOCATION: (316)
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    TYPE: DNA
289 TTCTTTATTCATCTCTGTTGAAGCCTANAAAAACCAAAACAAGCTGGTTGTGGTTC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR APPLICATION NUMBER: 60/202,084
RR FILLING DATE: 2000-05-04
DR APPLICATION NUMBER: 60/206,201
RR FILLING DATE: 2000-05-22
DR APPLICATION NUMBER: 60/218,950
RR FILLING DATE: 2000-07-14
                                                                                         Local
                                 5 TTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACACAACAACCTAGAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/222,903
FILING DATE: 2000-08-03
APPLICATION NUMBER: 60/223,416
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-08-04
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ilarity 65.5%;
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                                                                     Score 25.2; DB Pred. No. 9.5; 0; Mismatches
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Search completed: May 11, 2003, 06:11:42
Job time: 63.3684 secs

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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BM575510 170006871	BQ968546 QHB34E11. AZ652445 1M0525J11	AG025881 Homo sapi	AL777174 AL777174		Description

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AQ225617	AW781100	BF079516	BM784926	BQ488731	BG895557	R34801	BG467453	BQ939668	AZ539154	BE884936	BH828901	BH823752	AW085143	CNS05RVV	8	BF794977	BG617584	AZ248833	AZ312818	AV705148	AQ898421	BI903774	BQ616770	BM155751	BM037729	438	BF156127	AQ685997	BH714488	BQ745595	BI917143	AA757510	AZ407729	BG461281	BQ963329	47	382	BM617342
AQ225617 HS_2003_B	AW781100 sl89a10.y	BF079516 230139 MA	BM784926 K-EST0063	BQ488731 68-E8456-	5557 359	R34801 yh87e02.r1	BG467453 Na_L3_04A	BQ939668 AGENCOURT	AZ539154 ENTDD54TF	4936 60150687	8901 BACPP28	752	5143	1076 '	_	60225687	60261507	RPCI-23-	_	AV705148 AV705148	L HS 3135	-	6770 faa94h07		7729	4388	f147h10.	5997	H714488	59	714	N	772	_	29	94741 saj20e0	22 zf53f	BM617342 170006871

ALIGNMENTS

FEATURES source		TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BG294121/c LOCUS DEFINITION
http://image.lini.gov Plate: LiAM10372 row: k column: 22 High quality sequence stop: 718. Location/Qualifiers 1. 901	Email: cgapbs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 901) NIH-MGC http://mdc.nci.nih.gov/.	mRNA sequence. BG294121 BG294121.1 GI:13054439 EST. house mouse.	BG294121 901 bp mRNA linear EST 21-FEB-2001 602390986F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502925 5',

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AL777174 XGC-gastrula Silurana
mRNA sequence.
AL777174
AL777174 GI:21562878
                                                                                                                                                                                                                                                                                                                                                  This sequence is from a Xenopus Gene Collection constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                  Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas081f17.plkSP6
Sequencing_primer: PIKSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Taylor R
Sanger Centre
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinxton,
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/clome="IMAGE:4502925"
/clome=lib="NIH_MGC_94"
/tissue_type="retina"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Drimed unidirectionally; oligo-dT primed.
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
34 a 195 c 204 g 268 t
                                                                                                                       /dev stages "gastrula" (stages 10.5-13 mixed) "
/lab_host="Bscherichia coli XL1-blue"
/note="Vector: pCG107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                    into pCS107 with EcoRI at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire,
                                                                                                                                                                                                                                                                            /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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                                                                                                                                                                                                                                      clone_lib="XGC-gastrula"
                                                                                                                                                                                                                                                            /clone="TGas081f17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                             Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                        Helianthus annuus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                        QHB34E11.yg.abl QH_ABCDI sunflower clone QHB34E11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Medicine, Molecular Biology; 35 Shinanomachi, Shi
160-8582, Japan (B-mail:nshinizu@dmb.med.keio.ac.jp,
Tel:81-3-3351-2370)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 526)
Shimizu,N. and Asakawa,S.
The BAC end sequence of Homo sapiens BAC published Only in DataBase (1999)
2 (bases 1 to 526)
Shimizu,N. and Asakawa,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
               http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                          BQ968546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-DEC-1999) Nobuyoshi Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG025881.1 GI:6624572
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KB1562D12, genomic
                                                                                                                                                                                                                                       common sunflower.
                                                                                                                                                                                                                                                                        BQ968546.1
                                                                                                                                                                                                                                                                                                                                           BQ968546
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                                                                                                                                                    Heliantheae, Helianthus.
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                                                                                                                                 (bases 1 to 472)
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Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="KB1562D12"
/clone lib="KEIO BAC library"
/note="This sequence is reverse
KB1562D12"
1 146 c 90 g 178 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                                                                                                                                                                        GI:22386067
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71.7%;
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Pred. No. 20;
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VERSION
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FEATURES
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mes 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTACATCATTAAACACCTTTGAAGTAGCATAGATAACCNACATATGAAGAGAGA
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546 bp DNA linear GSS 14-DEC-200
1M0525J11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0525J11 R, DNA sequence.
                              Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: J column: 11
                                                                                                                                                                                                                            Contact: Robert B. Weiss University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedereen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OH_CA_Contig1526, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asmundson Hall, UCD,
Tel: 1-(530)-742-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                  plasmid inserts
                                                                                                                                                                                                            308,
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801 585 7177
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                 quality sequence stop: 546
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                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBRcDNASfiAB; The library was constructed
from 11 different sources of RNA from a single genotype.
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/lab_host="E.coli"
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cultivar="RHA801"
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clone="QHB34E11"
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Pred. No. 6
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DEFINITION
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BM575510/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
Eukaryota; Metazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17000687161198 A.Gam.ad.cDNA.blood1
19600449696818 5', mRNA sequence.
BM575510
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                                                                                                                                                                                                      Email: HoltRA@celera.com
                                                                                                                                                                                                                                                                                  45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                  Celera Genomics
                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African malaria mosquito.
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                                                                                                                                                                                       primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated this derivative of plasmid R1. The vector was ligated with agarded the contractive of plasmid R1. The vector was ligated with agarded the contractive of plasmid R1. The vector was ligated with agarded the contractive of plasmid R1. The vector was ligated with agarded the contractive of plasmid R1. The vector was ligated with agarded the contractive of plasmid R1.
                                                               chromosome) "
                   /db_xref="taxon:7165"
/clone="19600449696818"
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                                                                                        organism="Anopheles gambiae"
/strain="RSP-ST (Reduced susc. to Permethrin -
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
note="Vector: PWD42nv; Purified genomic DNA from M.
nusculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="UUGC1M0525J11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:18863977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%;
72.9%;
_lib="A.Gam.ad.cDNA.blood1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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); Mismatches
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RESULT 7
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 92
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTAAGCACTTGTGTAGTAGCTTAGAAAACCCAACAACAACCTAGAGGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM617342.1 GI:18915564
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BM617342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: HoltRA@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celera Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                      /note-"Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. CDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" 154 C 168 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Research Resource Center (www.malaria.mr4.org)" 155 c 143 g 184 t
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Anopheles gambiae"
/strain="RSP-ST (Reduced susc
chromosome)"
                                                                                                                                                                                                                                                                                       /clone="19600449731920"
/clone_lib="A.Gam.ad.cDNA.blood1"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%;
                                                                                       42.9%;
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A.Gam.ad.cDNA.bloodl Anopheles gambiae
5', mRNA sequence.
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                                                                    Score 27; DB Pred. No. 92; 0; Mismatches
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Pred. No. 91;
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MEDLINE
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                                                                                                      Query Match
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347
                                                                                       Local
                               7 ATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACCAACAACCTAGAGGATCCCCG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read
The vector to vector length is 1104
Insert Length: 2734 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasee, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkin, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA053822 514 bp mRNA li
zf53f01.rl Soares retina N2b4HR Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 514)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE:380665 5', mRNA sequence.
                                                                                       Similarity
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                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
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                                                                                     42.2%;
66.7%;
                                                                 Score 26.6; UB 2,
Pred. No. 1.2e+02;
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                                                                                                      Length 514;
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                                                                                                                                                                      TTTTTTTTTAAGCAATTGTTCTGTACATTAAATTACAAGCACAACAAC 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong strand This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Wector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            old
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue type="Leaf and shoot tip, salt stressed, ld seedling"
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db_xref="taxon:3847"
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71.4%;
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Pred. No. 1.2e+
0; Mismatches
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REFERENCE
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BG461281
LOCUS
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1 (bases 1 to 343)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,B., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Bittechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                      BG461281 343 bp r
RST44060 Athersys RAGE Library Homo
BG461281
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 843)
                    Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                    BG461281.1
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Similarity 66.7%;
38; Conservative
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14074 row: e column: 06
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                                    Contact: Scott J. Cain
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Carnegie Ave, Cleveland, OH 44115, USA
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//db xref="taxon:10090"
//dlone="IMAGE:5608493"
//clone=1ib="NHI_MGC_134"
//tissue_type="undifferentiated limb"
//tissue_type="undifferentiated limb"
//lab_host="MHIOB (phage-resistant)"
//note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
//note="Vector: pCMV-SPORT6.1.ccdb; Primer: Oligo dT. Average
insert size 1.7 kb. Constructed by ResGen, Invitrogen
Corp. Note: this is a NIH_MGC Library."
14 a 204 c 191 g 233 t 1 others
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Pred. No. 1.2e+02;
0; Mismatches 19;
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36; Conserv
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IM0178002R Mouse 10kb plasmid UUGCIM library

clone UUGCIM0178002 R, DNA sequence.

AZ407729

AZ407729 GI:10531742
                                                                                                                                                                                                                                                                              High quality sequence stop: 501.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0178 row: O column: 02
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 501)
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801 585 7177
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Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

81 c 46 g 81 t
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWP42nv; Purified genomic DNA from M.
musculus GS7BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0178002"
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/cell_line="HT1080"
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/db_xref="taxon:9606"
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                                                                                                                                          clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 1.4e+02;
D; Mismatches 16
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AA757510/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 38)

Hillier,L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zg37a09.sl Soares pineal_gland_N3HPG Homo sapiens
IMAGE:395512 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham
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                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 353.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored me DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampiallin resistance."
      0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
into the Not I and Ec (Pharmacia). Library
                                                                                                                                                                                                                                                  organism="Homo sapiens"

/db_xref="GDB:1301414"

/db_xref="taxon:9606"
                                                                                                                                                                                                                                clone="IMAGE:395512"
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Pred. No. 1.4e+02;
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RESULT 15
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Best Local Similarity
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                                                                                                                                                        5 TTATTTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATC 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
BQ745595 762 bp mRNA linear UI-M-EW0-bxh-g-17-0-UI.rl NIH_BMAP_EW0 Mus musculus IMAGE:5708200 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI917143 750 bp mRNA linear EST 16-OCT-2001 603181563F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245646 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BI917143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nttp://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                              0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                    Site 2: ECORV (destroyed); RNA source anonymous pool of fetal brains, female age 20 weeks, fetal age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                       0.7-3.5 kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5245646"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
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db_xref="taxon:9606"
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Pred. No. 1.7e+02;
0; Mismatches 18;
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Pred.
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                                                                                                                                                                                                                                                                                                                    tracking code 017. Note:
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Job time

Search completed: May 11, 2003, 04:54:18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
  490
                                                                                                     Local
                                    9 TTAAGCACTTGTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGGATCCCCG 63
TCAAGCACTTAATTAATAATTCACAAAACCACACAAACCATCCATGCACG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BQ745595.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                   Similarity
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                                                                                                                                                                                       171 a
                                                                                                                                                                                                                                                                                                                                         clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                              University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Healt (NIMH), Hemin Chin, Ph.D., program coordinator."

148 c 198 g 244 t 1 others
                                                                                                                                                                                                                                                                                     ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                41.6%;
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                                                                               Score 26.2; DB 14;
Pred. No. 1.7e+02;
0; Mismatches 18;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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| SIDS2/gcgdata/genesed/geneseqn-emb1/NA1991.DAT: |
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\SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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score greater t Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

	88.6 541 21 88.1 393 21	21	94.9 296	94.9 259 21	100.0 79 21	100.0 79 21	Score Match Length DB ID
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AAT32299 AAH28368 AAW99491 AAX86466 AAC89658	AAU39442 AAC83764 AAH28369 AAV99492 AAQ23533 AAQ25080 AAQ72688	AAD03395 AAD03402 AAD10066 AAA71895 AAC87192	AAD03396 AAD03397 AAD03398 AAD03394 AAD03421 AAA96847 AAA96471 AAA96463 AAA96463 AAA96460 AAD03420 AAD03420 AAD03400 AAD03400 AAD03400 AAD03400	AAA96855 AAA96857 AAA96839 AAAD03420
Cauliflower mosiac Nucleotide sequenc Sequence containin 35S CMV promoter s Tomato spotted wil	Caulillower mosaic Plasmid pMON295 Ca Nuclectide sequenc Cauliflower mosaic CaMV35S promoter (CAMV 35S promoter, Camliflower mosaic	Mpr1131 promoter D MPr1139 promoter D Amplified product Soybean RRS gene N CaMV35S promoter e	promote promote promote promote promote promote promote ide sequ ide sequ ide sequ ide sequ promote promote promote	Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc CaMV as -2/as-1 PCR

ALIGNMENTS

RESULT 1 AAA96848

AAA96848 standard; DNA; 79

AAA96848;

19-FEB-2001 (first entry)

Directional desoxynucleotide building block S7.

Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; ss.

Synthetic.

WO200058485-A1

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370

29-MAR-1999; 99FR-0003925

Rance I, (MERI-) MERISTEM THERAPEUTICS Gruber V, Theisen M;

WPI; 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises

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Best I
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 The present sequence represents the directional building block S7, which is used to construct chimeric promoters of the invention in PCR reactions. The specification describes a chimeric expression promoter comprising a petE promoter of the pea plastocyanin gene,
                                                                                                         Chimeric expression promoter for producing dicotyledonous and monocotyledonous transgenic plants comprises a nucleic acid suderived from a promoter of the pea plastocyanin gene -
                                                                                                                                                                           WPI; 2000-587667/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                            petE
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                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter; chimeric promoter; transgenic plant; MPr1108;
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                                                                            Page
                                                                                                                                                                                                      Gruber V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directional building block S7.
                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer;
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Pred. No. 5.2e-20;
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Best Local
                         promoter is derived from the petE promoter from pea plastocyanin gene, by fusing the petE as-1 like and nos enhancer like elements to the promoter MPr1098 (comprising TATA and CAAT boxes of petE), and then fusing a fragment comprising a duplication of the element as2 and as1. The petE promoter directs cell-specific but not full light-regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a Box operably or functionally linked upstream of a CAAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, wheat
rape, be barley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a G box operably or functionally linked upstream of a CAAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn
                                                                                                                                                                                                                                                                                             Chimeric expression promoter for producing dicotyledonous monocotyledonous transgenic plants comprises a nucleic aci derived from a promoter of the pea plastocyanin gene -
                                                                                                                                                                                                                                  The present sequence represents the chimeric promoter Mpr1112. The
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plastocyanin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA96477 standard; DNA; 259
                                                                                                                                                                                                                                                                Claim 25; Page
                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the promoter MPr1112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-PEB-2001
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               .g. potato, to
ape, beetroot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGATGACGCATGCCACT 79
                                                                                                                                                                                                                                                                                                                                                           2000-587667/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGATGACGCATGCCACT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA
                                                                                                                                                                                                                                                                                                                                                                                                                      MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                      Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
 rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99FR-0003635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric promoter;
                                                                                                                                                                                                                                                               79; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter;
                 sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                                                                                                        Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79;
Pred. No.
                 and monocotyledonous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                           a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant; MPr1112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                             sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cotton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 4
AAA96465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
Best Local Similarity
                                                                                      promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a gromoter of the pea plastocyanin gene, or comprising a G box operably or functionally linked upstream of a CAAT box. TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
                                                                                                                                                                                    The present sequence represents the chimeric promoter Mprilli. The promoter is derived from the petE promoter from pea plastocyanin gene, by fusing the petE as-1 like and nos enhancer like elements to the promoter Mprilose (comprising TATA and CAAT boxes of petE), and then inserting a G box and fusing a fragment comprising a duplication of the element as2 and as1. The petE promoter directs cell-specific but not full light-regulated expression in transgenic tobacco plants. The
                                                                                                                                                                                                                                                                                                                      Chimeric expression promoter for producing dicotyledonous monocotyledonous transgenic plants comprises a nucleic aci derived from a promoter of the pea plastocyanin gene -
                                                                                                                                                                                                                                                                                                                                                                                                       Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      petE promoter; chimeric promoter; transgenic plant; MPr1111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA96465 standard; DNA; 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                        Sequence 296
                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587667/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2000; 2000WO-IB00317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prastocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA96465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI-) MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGACGCATGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGACGCATGCCACT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGG 72
                                                                               beetroot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                       Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
                                        B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                              71; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter; ss.
                                                                 ö
                                                                              sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                       A; 74 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the promoter MPr1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
94.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                       Theisen M;
                                                                 corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75;
Pred., No.
Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 G;
                                       45 G; 83
                                                                              and monocotyledonous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 T; 0 other
                                       T; 0 other;
DB 21; 1
2.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4e-18;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 259;
           Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                            species, e.g. wheat
                                                                                                                                                                                                                                                                                                                                    acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                     sequence
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RESULT 5
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                                                                                           Matches
                                                                                                                      Query Match
                                                                                                                                                                                            The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Commelina yellow mot
Chimeric - Cassava vein mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus;
                                                                                                                                                      Sequence 472
                                                                                                                                                                                                                                                                                                                                     The present sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 88; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic plant; chimera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of chimeric expression promoter MPr1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA96859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96859 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI-)
                               306
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                                                                                                         Local
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AGGGATGACGCATGCCAC 78
                               CTTGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA
                                                            CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGACGCATGCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGACTAGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Commelina yellow mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                         Conservative
                                                                                                                                                    BP; 149 A; 92 C; 112 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                  transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99FR-0003925
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                                                                                                         88.6%;
93.6%;
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                                                                                           <u>,</u>
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                                                                                                         Score 70; DB 21;
Pred. No. 2.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                      Length 472;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                         Gaps
                                                              60
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RESULT 7
AAA96853
ID AAA9
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AAA96858
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                                                                                                                                                        Query Match
Best Local
                                                                                                                                            Matches
                                                                                                                                                                                                                  The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                         Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeria expression promoter; plant vascular expression promoter; plant green tissue expression promober; Cassava vein mosaic virus transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-2001
                                                                                                                                                                                     Sequence 541
                                                                                                                                                                                                                                                                                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Commelina yellow mottle virus.
Chimeric - Cassava vein mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA96858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA96858 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of chimeric expression promoter MPrl168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promoter; intergenic region; Commelina yellow mottle virus;
                                                      366
                                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AGGGATGACGCATGCCAC 383
                                                                           61
                                                                                                                                                     Local
                                                                                                                      μ
                                                                                                                                                                                                           producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                      2000-647238/62
                                                      AGGGATGACGCATGCCAC 383
                                                                                                 CTTGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA 365
                                                                                                                     CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA 60
                                                                          AGGGATGACGCATGCCAC 78
                                                                                                                                            1 Similarity 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                          Page 87-88; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gruber V,
                                                                                                                                          88.6%;
llarity 93.6%;
Conservative
                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99FR-0003925.
                                                                                                                                                                                     169 A; 104 C; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                           Score 70; DB 21;
Pred. No. 2.2e-16;
D; Mismatches 5;
                                                                                                                                                                                     G; 138 T; 0 other;
                                                                                                                                                                Length 541;
                                                                                                                                            Indels
                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus;
                                                                                                                                            Gape
                                                                                                                                            0
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AAA96853 standard; DNA; 393

₽P

Nucleotide sequence of chimeric expression promoter MPrll63.

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RESULT 8
AAA96854
ID AAA9
XX
AC AAA9
AC AAA9
XX
DT 19-F
XX
DE Nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric expression promoter; plant green tissue expression transgenic plant; chimera; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Commelina yellow mottle virus. Chimeric - Cassava vein mosaic virus.
                                                                                                          AAA96854;
                                                                                                                                                  AAA96854 standard; DNA; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 85; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647238/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rance I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2000; 2000WO-IB00370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200058485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of chimeric expression promoter MPr1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2001
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                                                                19-FEB-2001
                                                                                                                                                                                                                                                             287
                                                                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing
                                                                                                                                                                                                                                                                                                   GGATGACGCATGCCAC
                                                                                                                                                                                                                                                                                                                                               TGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG
                                                                                                                                                                                                                                                                                                                                                                            TGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG
                                                                                                                                                                                                                                                             GGATGACGCATGCCAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.1%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 75 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theisen
                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69.6; DB 21
Pred. No. 2.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant vascular expression promoter; promoter; Cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 393;
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AAA968A

ID AAA9

AC AAA9

AC AAA9

XX NOC NUCL

XX NOC NUCL

XX Prom

KW Prom

KW Prom

KW Chim

KW Plan

XX Chim

OS Chim
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                              Promoter;
chimeric e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric expression promoter for transgenic plant production, compris-
sequence from promoter comprising vascular expression region replaced
with sequence from promoter comprising green tissue expression region
 Chimeric -
Chimeric -
                                             chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; chimera; ss.
                                                                                                                             Nucleotide sequence of chimeric expression promoter MPr1165
                                                                                                                                                             19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a commerce promoter or the specification describes chimeric expression promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus transgenic plant; chimera; ss.
                                                                                                                                                                                                                           AAA96856 standard; DNA; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2000; 2000WO-IB00370
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                                                                                                                                                                                                                                                                                                            287
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                                                                                                                                                                                                                                                                                                          GGATGACGCATGCCAC
                                                                                                                                                                                                                                                                                                                                        GGATGACGCATGCCAC 78
                                                                                                                                                                                                                                                                                                                                                                        TGGTTACGACTAGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG 286
                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Page 86; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
72; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462
                                                                                            intergenic region; Commelina yellow mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassava vein mosaic virus.
                Commelina yellow mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a chimeric promoter of the invention cation describes chimeric expression promoters. These
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99FR-0003925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 A; 87 C; 111 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.1%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theisen M;
                                                                                                                                                                                                                                                                                                          302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plants.
                                                                                                                                                                                                                             ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.6; DB Pred. No. 3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Cassava vein mosaic virus

29-MAR-2000; 2000WO-IB00370

05-OCT-2000.

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RESULT 10
AAA96855/c
ID AAA96855/c
XX AAA96
XX AAA96
XX I9-FE
XX Nucle
XX Promc
KW Promc
KW Chime
KW plant
KW plant
KW plant
KW plant
KW plant
KW Chime
COS 
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Best Local S
Matches 72
                                                                                                                                                                                         Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.
                                                                                                                                                                                                                                                                                             Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric expression promoter for transgenic plant production, c sequence from promoter comprising vascular expression region re with sequence from promoter comprising green tissue expression
                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of chimeric expression promoter MPr1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 600
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The specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2000; 2000WO-IB00370
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                                                                                                                                                                                                                                                                         transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTTACGACTAGTGATGTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                            1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruber V,
                                                                                                                                                                                            Cassava
                                                                                                                                                                                                                      Commelina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a chimeric promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 188 A; 111 C; 147 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99FR-0003925
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                                                                                                                                                                                                                                                                            chimera; ss
                                                                                                                                                                                            vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.1%;
                                                                                                                                                                                                                      yellow mottle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392
                                                                                                                                                                                            mosaic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.6; DB 21; Pred. No. 3.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600;
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RESULT 11
AAA96857
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Best Local Similarity
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sequence
with sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                       Rance I,
                                                                                                                                                                                 Chimeric -
                                                                                                                                                                                                                   chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; chimera; ss.
                                                                                                                                                                                                                                                                                                                 19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                AAA96857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 392
                                                                          29-MAR-1999;
                                                                                                                              05-OCT-2000
                                                                                                                                                       WO200058485-A1
                                                                                                                                                                                                                                                                                   Nucleotide sequence of chimeric expression promoter MPr1167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
                                                                                                   29-MAR-2000; 2000WO-IB00370.
                                                                                                                                                                                                                                                            Promoter; intergenic region; Commelina yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-1999;
                                                 (MERI-) MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eric expression promoter for transgenic plant production, comprises ence from promoter comprising vascular expression region replaced sequence from promoter comprising green tissue expression region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-647238/62
                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGAC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                  standard;
                     Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruber V,
                                                                                                                                                                               Cassava ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a chimeric promoter of the invention cation describes chimeric expression promoters. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.3%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          вÞ;
                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                  234
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                          99FR-0003925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99FR-0003925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 A; 80 C; 87
                                                                                                                                                                                 vein
                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                             yellow mottle virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theisen M;
                       Theisen M;
                                                                                                                                                                                                                                                                                                                                                                  604
                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ore 69; DB
ored. No. 4.8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; I
4.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                            mottle virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Loc
Matches
                                Query Match
                                                                                                           The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
                                                                                                                                                                                                                                                                                                                                             Chimeric expression promoter for transgenic plant production, compris sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
                                                                Sequence
                                                                                                                                                                                                                                                 The
The
                                                                                                                                                                                                                                                                                                  Claim
                 Local
                                                                                               producing
                                                                                                                                                                                                                                                                                                  5
 70;
                 Similarity
                                                                  604
                                                                                                                                                                                                                                                                                               Page 87; 91pp; English.
 Conservative
                                                               BP; 186
                                                                                               transgenic plants.
                                                                                                                                                                                                                                                 represents a chimeric promoter of the invention
               95.9%;
                                                                A; 116 C;
 ٥,
               Score 68.2; DB 21; Pred. No. 1.1e-15;
Pred. No. 1.10); Mismatches
                                                                  145
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                                                                  157
                                                                Η,
                                                               0 other;
                                Length
   Indels
   0
                                                                                                                                                                                                                                                                                                                                                                               comprises
Gaps
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RESULT 12
AAA96839
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AAA96839 standard;
                                                             436
                                                                                                               376
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                                                             TGACGCATGCCAC
                                                                                    TGACGCATGCCAC
                                                                                                               TGCCACCTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA
                                                                                                                                       TGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA
                                                             448
                                                                                      78
DNA;
371
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chimeric expression promoter; plant vaso
plant green tissue expression promoter;
transgenic plant; chimera; ss.
  Chimeric -
                                                                                                                      Promoter; intergenic region; Commelina yellow mottle virus;
                                                                                                                                                              Nucleotide sequence of chimeric expression promoter MPr1146
                                                                                                                                                                                                        19-FEB-2001
                                                                                                                                                                                                                                                AAA96839;
  Cassava
                       Commelina
                                                                                                                                                                                                        (first
  vein
                                                                                                                                                                                                      entry)
                       yellow mottle virus.
mosaic virus.
                                                                                                       vascular expression
                                                                                  Cassava vein mosaic virus;
                                                                                                     romoter;
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WO200058485-A1.
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05-OCT-2000.
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29-MAR-2000; 2000WO-IB00370
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29-MAR-1999;
99FR-0003925
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(MERI-) MERISTEM THERAPEUTICS

Rance I, Gruber V, Theisen

2000-647238/62

Chimeric expression promoter for transgenic plant production, comprise sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region comprises

Claim 5; Page 81; 91pp; English

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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a chimeric promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter; in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originate from the Cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful
The patent discloses chimeric expression promoters comprising nucleic acid sequences derived from the promoters of genes encoding high molecular weight wheat glutenin proteins. The chimeric promoters are used in standard recombinant DNA techniques for the generation of transgenic plants and the production of polypeptides (e.g. marker and therapeutic polypeptides).

The present DNA sequence is a PCR primer comprising the cauliflower mosaic virus (CaMV) 35S promoter as-2 motifs (in duplicate) and as-1 motif, used in the construction of the wheat high molecular weight
                                                                                                                                                                   Chimeric expression promoters comprising nucleic acids from genes encoding a high molecular weight wheat glutenin proteins, useful in the production of transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cauliflower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheat; glutenin; CaMV 35S promote:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD03420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                            Example 3;
                                                                                                                                                                                                                                                                                                               30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                       05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                 WO200123593-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CaMV as-2/as-1 PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD03420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCCACT
                                                                                                                                                                                                                               2001-245005/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conserv
                                                                                                                                                                                                                                                                                    MERISTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                                                                         Norre
                                                                                                                                          Page 32; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                              99FR-0012373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic plant; PrHMWG-Dx5;
r; as-2 motif; as-1 motif; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                        Ρ,
                                                                                                                                                                                                                                                                                     THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer #1 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.1%;
                                                                                                                                                                                                                                                         Theisen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 89 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for constructing MPr1130 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21,
3. 1.1e-15;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant promoter originates
y, the promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPr1130 primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
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RESULT 14
AAD03396
ID AAD03
AC AC AAD03
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plasmids
                                                  and therapeutic party in the present DNA sequence is MPr1133 promoter which is derived by The present DNA sequence is MPr1133 promoter which is derived by deleting the sequence (comprising 2 prolamine-like boxes, 2 GATA boxe G-box and activating element) located upstream of the nucleotide -197 of MPr1130 promoter (AAD03394). The MPr1130 promoter is derived from wheat high molecular weight glutenin PrHWWG-DX5 promoter DNA (AAD03394) wheat high molecular weight glutenin PrHWWG-DX5 promoter DNA (AAD03394).
                     Note: The
                                                                                                                                                                                                                           The patent discloses chimeric expression promoters comprising nucleic acid sequences derived from the promoters of genes encoding high molecular weight wheat glutenin proteins. The chimeric promoters are used in standard recombinant DNA techniques for the generation of transgenic plants and the production of polypeptides (e.g. marker
                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric expression promoters comprising nucleic acids encoding a high molecular weight wheat glutenin proteir production of transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_signal
                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 116; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-245005/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wheat; glutenin;
CaMV 35S promote:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mpr1133 promoter DNA derived from wheat glutenin MPrHMWG-Dx5 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD03396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GTGATTGATGTGATATCAAGATTGATGTTGATATCTCCACTGACGTAAGGGATGACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERISTEM THERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
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                     present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norre F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
Cauliflower mosai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
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Conservative 0;
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the sequence listing

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Rest Local
                      The patent discloses chimeric expression promoters comprising nucleic acid sequences derived from the promoters of genes encoding high molecular weight wheat glutenin proteins. The chimeric promoters are used in standard recombinant DNA techniques for the generation of transgenic plants and the production of polypeptides (e.g. marker and therapeutic polypeptides).

The present DNA sequence is MPr1134 promoter which is derived by deleting the sequence (comprising 2 prolamine-like boxes, 2 GATA boxes and G-like box) located upstream of the nucleotide -260 of MPr1130 promoter (AADO3394). The MPR1130 promoter is derived from wheat high molecular weight glutenin PrHMWG-Dx5 promoter DNA (AADO3390) and contains elements from the cauliflower mosaic virus (CaMV) 35S
                                                                                                                                                                                                                                            Chimeric expression promoters comprising nucleic acids from genes encoding a high molecular weight wheat glutenin proteins, useful in the production of transgenic plants -
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Chimeric -
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             promoter
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Note: The present sequence is referred as SEQ ID NO: 8 throughout the
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Cauliflower mosaic virus.
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ន្តន្តន S Matches Query Match Best Local & specification. However this sequence is shown as SEQ the sequence listing. Sequence 299 BP; 78 A; 87 C; Local 15 GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72 58; Conservative Similarity 73.4%; Sur 100.0%; Pr Score 58; Pred. No. 49 G; Mismatches 85 T; 0 other; DB 22; 5.7e-12; Length 299; Indels ID NO: 0 36 in Gaps

0

Search completed: May 11, Job time : 154.644 secs 2003, 03:04:04 밁

138

GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 195

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Pred. No.
is the number of results predicted by chance to have
                                            em_htgo_other:*
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em_htg_hum: *
em_htg_inv: *
em_htg_other: *
em_htg_mus: *

em_pat:*
em_ph:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. a a a a a 39.22 20.22 20.22 20.22 20.22 20.22 69.69.6 89 Query Match 멂 AX103756 AX103757 AX103758 AX103763 AX103776 AX036610 AX036747 AX036601 AX036741 AX036740 AX036757 AX036739 AX036759 AX036758 AX036753 AX036611 AX036748 AX036616 AX093052 AX036755 AX036756 AX093047 IJ I04847 AX405116 AX164073 AX103781 AX103753 AX036754 AX036603 ARCAMVPH ALIGNMENTS AR434749 Zea mays AX164073 Sequence AR434747 Zea mays AR434746 Zea mays AR434746 Zea mays AR734750 Zea mays AR7334750 Zea mays AX033493 Sequence AX044092 Sequence AX044092 Sequence BD001990 A transge E01311 Cauliflower 104847 Sequence 3 AX036611 Sequence AX036748 Sequence AX036616 Sequence AX036603 Sequence AX036759 Sequence AX036759 Sequence AX036754 Sequence AX036754 Sequence AX036755 Sequence AX036755 Sequence AX036755 Sequence AX036757 Sequence AX036757 Sequence AX103782 Sequence AX103783 Sequence AX103784 Sequence AX103784 Sequence AX103755 Sequence AX103756 Sequence AX103756 Sequence AX103751 Sequence AX036741 Sequence AX036741 Sequence AX036741 Sequence AX036741 Sequence AX036741 Sequence AX036745 Sequence AX103756 Sequence AX103758 Sequence AX103758 Sequence AX103758 Sequence AX103758 Sequence AX103759 Sequence AX103759 Sequence AX103759 Sequence AX103759 Sequence AX103759 Sequence Description X04879 CaMV promot sequence sequence

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

GenEmbl:*
1: gb_ba:*
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em_ba:*

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

4109280

2054640 seqs, 14551402878 residues

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

Title: Perfect score:

US-09-963-803-14 79

catgctgcagactagtgatt.....aagggatgacgcatgccact

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May 11, 2003, 02:50:55; Search time 836.727 Seconds (without alignments) 2747.757 Million cell updates/sec

Sequence:

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95

OM nucleic - nucleic search, using sw model

Copyright

GenCore version 5.1.5 (c) 1993 - 2003 Compugen

Ltd.

FEATURES	JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX036611	RESULT 1
Location/Qualifiers	Patent: FR 2791358-A 17 29-SEP-2000;	Rance.I., Theisen.M. and Gruber.V.	1 (bases 1 to 79)	artificial sequences.	synthetic construct	synthetic construct.		AX036611.1 GI:11226206	AX036611	17 from Patent F	AX036611 79 bp DNA	•	
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RESULT 3
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Patent: FR 2791358-A 27
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synthetic construct
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to 79)
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Rance I., Theisen, M. and Gruber, V.
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                                               synthetic construct.
                                                                                 AX036616.1
                                                                                             Sequence 22 from Patent AX036616
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/note="birectional building block S7~Directional building block oligonuclectide for the construction of promoters by lb-pck"
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                                RESULT 5
AX036759
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AUTHORS
JOURNAL
            DEFINITION
ACCESSION
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AX036603
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AX036759
Sequence 25
AX036759
AX036759.1
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65 ATGACGCATGCCACT
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Rance, I., Theisen, M. and Gruber, V.
Patent: FR 2791358 A 9 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               artificial sequences.
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75; Conservative
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a 67 c 38 g 72 t
25
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1 74 c 45 9
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/db_xref="taxon:32630"
1. ..259
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                                                                                                                                                                                                                                                                                                                                                             /note="Promoter MPr1111 created by inserting at position of MPr1098, an 18 bp element containin and fusing a sequence of 58 bp (duplication of
                                                                                                                                                                                                                                                                                                                                                                                                                                organism="synthetic construct"
/db_xref="taxon:32630"
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; Pred. No. 3.4:
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J. 3.4e-16;
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ining a 'G'
                  16-NOV-2000
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TITLE
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Best Local Similarity
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366
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                           AGGGATGACGCATGCCAC 78
                                                      CTTGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA 365
                                                                        CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA 60
AGGGATGACGCATGCCAC 383
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synthetic construct
artificial sequences.
1 (bases 1 to 472)
1 (bases 1 to 472)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 25 05-OCT-2000;
                                                                                                                                                                                                                                                                                    Chimeric expression promoters originating from commelina mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 24 05-OCT-2000; MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); THEISEN MB; GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 541)
Rance, I., Theisen, M. and Gruber, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 from Patent WO0058485. AX036758
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/db_xref="taxon:32630"
/note="promoter MPr1168"
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/db_xref="taxon:32630"

/note="promoter MPr1169"
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Pred. No. 2.1e-14;
0; Mismatches 5
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                                                                                                             Score 70; DB 6;
Pred. No. 2.1e-14;
0; Mismatches 5
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RESULT 7

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63 GGATGACGCATGCCAC 78

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AX036754
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TGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG
                          TGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG 62
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AX036753
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Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                                                                                                                                                           1 (bases 1 to 462)
Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 20 05-OCT-2000;
MERISTEM THERAPEUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
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Sequence 20 from Patent
AX036754
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/db_xref="taxon:32630"
/note="promoter MPr1162"
                                                                                                                  /organism="synthetic construct"
/db xref="taxon:32630"
/note="promoter MPr1163"
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75 c
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94.7%;
                                                               88.1%;
94.7%;
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                                                  Score 69.6; DB 6;
Pred. No. 2.9e-14;
0; Mismatches 4
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WO0058485
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BASE COUNT
ORIGIN
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ORGANISM
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AX093047
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AX036756
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                                            BASE COUNT
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                                                                                                                                                                                 synthetic construct.

synthetic construct
artificial sequences.
1 (bases 1 to 9285)
Gruber, V. and Comeau, D.
Synthetic vectors, transgenic plants containing the
for obtaining them
patent: WO 0118192-A 52 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATGACGCATGCCAC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCCACTGACGTAAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATGACGCATGCCAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTTACGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAG 286
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Sequence 22 from Patent
AX036756
                                                                                                                                                                                                                                                                                                                                            Sequence 52 from Patent AX093047 AX093047.1 GI:13509522
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Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPSUTICS (FR) , RANCE IANN (FR) ;
GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                  /note="pMRT1336 results from the insertion into pMRT1196 of the promoter MPr1165 isolated from plasmid pMRT1322 and described in PCT patent application PCT/IB00/00370" a 2252 c 2506 g 2087 t
                                                                                                                            /organism="synthetic construct"
/db_xref="taxon:32630"
/note="pMRT1336"
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/db_xref="taxon:32630"
/note="promoter MPr1165"
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88.1%;
94.7%;
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Score
Pred.
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Pred. No. 2.9e-14;
D; Mismatches 4,
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WO0118192.
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69.6; DB 6;
No. 2.8e-14;
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              Length 9285;
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SOURCE
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AX036755/c
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Sequence
AX036755
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Sequence
AX093052
                                  artificial sequences.

1 (bases 1 to 392)

Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 21 05-OCT-2000;
MERISTEM THERAPBUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
72; Conserv
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1 (bases 1 to 15077)

Gruber,V. and Comeau.D.

Synthetic vectors, transgenic plants containing them,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                               synthetic construct
                                                                                                                                                           synthetic construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="pMRT1342 results from the replacement of the expression cassette ep35S-gus-polyA35S from pMRT1335 the expression cassette L5-gus-polyA35S isolated from pMRT1336"
                                                                                                                                                                                                                21 from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 from Patent
                       Location/Qualifiers
organism="synthetic"
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/db_xref="taxon:32630"

/note="pMRT1342"
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Pred. No. 2.7e-14;
0; Mismatches 4;
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WO0118192.
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WO0058485
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                                                   THEISEN MANFRED (FR)
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AX036757
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AX036739
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                     TGACGCATGCCAC 78
                                                                                                                                                                                                                                                                              TGCCACCTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA 435
                                                                                                                                                                                                                                                                                             TGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA 65
                                                                                                                                                                                                                           TGACGCATGCCAC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
1 (bases 1 to 371)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 5 05-OCT-2000;
                                                                              synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 604)
Rance,I., Theisen,M. and Gruber,V.
Rance,I., Theisen,M. and Gruber,V.
Chimeric expression promoters originating from
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPSUTICS (FR); RANCE IANN (FR);
GRUBER VERONIQUE (FR)
                                                                artificial sequences.
                                                                                                                   AX036739 371 bp
Sequence 5 from Patent WO0058485.
AX036739 GI:11226248
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AX036757
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/note="promoter MPr1164"
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/db_xref="taxon:32630"
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1 (corre, F. and Theisen, M. Synthetic and chimeric promoters, 6
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GRUBER VERONIQUE (FR)
                                                                                                                                                                                                             vectors, transgenic plants and seeds for producing them patent: WO 0123593-A 34 05-APR-2001;
                                                                                                                                                                                                                                                                                                    synthetic construct
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/db_xref="taxon:32630"
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/db_xref="taxon:32630"
/note="promoter MPr1146"
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46, Appl
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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| cgn2_6/ptodata/1/ina/5A_COMB.seq:*
| cgn2_6/ptodata/1/ina/6A_COMB.seq:*
| cgn2_6/ptodata/1/ina/6A_COMB.seq:*
| cgn2_6/ptodata/1/ina/6B_COMB.seq:*
| cgn2_6/ptodata/1/ina/ETUS_COMB.seq:*
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US-08-711-728-3
US-08-764-100-23
US-09-042-426-1
US-09-291-238-1
US-09-330-737-1
US-09-330-714A-1
US-09-330-714A-1
US-09-330-714A-1
US-09-330-737-5
US-09-330-737-5
US-09-330-738-5
US-09-330-738-5
US-09-330-738-5
US-09-330-738-5
US-09-330-738-5
US-09-330-734A-5
US-08-371-764-1
US-08-450-834-5
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Sequence
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US-08-247-809A-3
                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 439 base pairs
TYPE: nucleic acid
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Query Match
Best Local Similarity 100.
Thes 39; Conservative
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                                                                                                                                                                                                                                                      STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inc
MEDIUM TYPE: Diskette, 3.50 inc
MEDIUM TYPE: Diskette, 3.50 inc
MEDIUM TYPE: Biskette, 3.50 inc
MEDIUM TYPE: Biskette, 3.50 inc
MEDIUM TYPE: Diskette, 3.50 inc
MEDIUM TYPE: Biskette, 3.50 inc
MEDIUM TYPE: WECTOWN
MEDIUM TYPE: OSE
COMPUTER: NEC POWETHATE 1 Plus
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING SYSTEM: US/08/247,8
FILING DATE: May 23, 1994
FILING DATE: May 23, 1994
CILING DATE: May 23, 1994
CILING DATE: May 23, 1994
CILING DATE: May 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: KUTT G. Briscoe
REGISTRATION NUMBER: Bayer
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Peter H. Schreier; Klaus Stenze.
APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                       ; Score 39; DB
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US-08-729-601A-43
US-09-363-970-35
US-09-011-151-9
US-08-729-601A-46
US-09-1185-244-2
US-09-471-913-6
US-09-471-913-6
US-09-478-993-2
US-09-458-993-2
US-09-655-999-6
US-08-2478-093-5
US-08-255-507-16
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Sequence Sequence

Sequence

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Result No.

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                                                                               Sequence 23, Application US/08764100 Patent No. $5773700
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Best Local Similarity
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                                                                 GENERAL INFORMATION:
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APPLICANT: Peter H. Sci
APPLICANT: Edgar Maiss
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DE 4:
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-MAY-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1
CURRENT, APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
                                                  APPLICANT:
                                                                                                                                                                                 338 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 376
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 03-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                            H: 439 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SPRUNG HORN KRAMER & WOODS
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (914) 332-1844
De Haan, Petrus T.
Gielen L., Johannes J.
Peters, Dirk
                                                van Grinsven J., Martinus
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                             49.4%; Score 39;
100.0%; Pred. No.
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Patent No. 6114608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 857-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/
FILING DATE: 17-MAR-1993
APPLICATION UMMBER: GB 92C
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Alle
REGISTRATION NUMBER: 34,45
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US/08/214,064
FILING DATE:
                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: No. 61146
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 354-3592
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                             FITLE OF INVENTION:
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FILING DATE:
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               APPLICATION NUMBER:
                                                                                                                                           COUNTRY: USA
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975 California Avenue
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857-1125
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DNA Construct
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Containing Ba
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6.2e-06;
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

NAME: Hoxie, Thomas REGISTRATION NUMBER:

Thomas

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GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
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TELEPHONE: (919) 541-8614
TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                    TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
            MOLECULE TYPE: DI
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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ADDRESSEE: No. 6222104artis Corporation
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CLONE: 35S Promoter
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CITY: Summit
STATE: New Jersey
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                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                   TOPOLOGY:
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                             DNA (genomic)
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100.0%; Pred., No. 6.6e-06;
live 0; Mismatches 0;
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RESULT 7 US-09-328-473-1

Sequence 1, Application US/09328473 Patent No. 6232533

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US-09-330-760-1
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                                                                                                                  US-09-330-760-1
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                                                         Matches
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Irvin
                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Summit
CITY: Summit
CITY: New Jersey
"""R: New Jersey
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
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APPLICATION NUMBER: 09
FILING DATE: March 13.
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MEDIUM TYPE: Floppy
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CLONE: 35S Promoter
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274 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 312
                  34 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
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(919) 541-8689
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ENTION: DNA Construct Containing Bacillus
                                                         Conservative
                                                                                                                                                                                         DNA (genomic)
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                                                 49.4%; or
100.0%; Pr
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Best Local Similarity
Matches 39; Conserv
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APPLICATION NUMBER: 09/042,
PILING DATE: MARCH 13, 199/
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Irvin
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[INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
         COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232534artis Corporation
STREET: 564 Morris Avenue
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REFERENCE/DOCKET NUMBER: 13:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Rel-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: No. 6232533artis Corporation
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                                                                                                                                                     CITY: Summit
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                                                                                                                                      New Jersey
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                                                                                                                                                                                                                                                              Irvin J.
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DNA Construct
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Construct Containing Bacillus
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Containing Bacillus
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RESULT 9
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION TARESTORM #1.25
                                                                                                  NAME: HOXI:, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 13:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/329,169 FILING DATE: 09-Jun-1999
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LENGTH: 532 base pairs
                                                                   TELEFAX:
                                                                                   TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07901
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                                                                   (919) 541-8689
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US-09-330-714A-1
                                                                                                      US-09-330-714A-1
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Patent No. 6342660
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
                                   Matches
                                                                  Query Match
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34 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
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                                                  Local Similarity
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APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                     ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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IMMEDIATE SOURCE:
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                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey COUNTRY: USA
                                                                                                                                        CLONE: 35S Promoter
                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hoxie, Thomas REGISTRATION NUMBER: 32,993
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                                49.4%; Score 39;
100.0%; Pred. No.
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Pred. No.
                                  Mismatches
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RESULT 12
US-09-042-426-5
US-09-042-426-5
Sequence 5, Application US/09042426
; Patent No. 6114608
; Patent No. 6114608
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US-09-328-826-1
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Best Local Similarity
Matches 39; Conserv
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                                                       GENERAL INFORMATION:
APPLICANT: Irvin J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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SEQUENCE CHARACTERISTICS:
                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                   274 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA
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ADDRESSEE: No. 6114608artis Corporation STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
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FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6399860artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Irvin J. Mett
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 35S Promoter NCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/328,826 FILING DATE: 09-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 564 Morris
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                  49.4%; DC
100.0%; Pr
                                                                           Mettler, Paul
DNA Construct
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DNA Construct Containing Bacillus
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                                                                                                                                                                                                                                                                                                                        Score 39; DB; Pred. No. 6.6
                                                                       S. Dietrich, Ralph Sinibaldi
Containing Bacillus
                                                                                                                                                                                                                                                                                                                                            DB 4; L
6.6e-06;
                                                                                                                                                                                                                                                                                                                                                           Length 532;
                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                          <u>.</u>
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COMPUTER READABLE FORM:

COUNTRY:

New Jersey

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RESULT 13
US-09-291-238-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Applic
Patent No. 6222104
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SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNMER: US/09/042,42. FILING DATE: March 13, 1998 CLASSIFICATION: 800
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Irvin J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 49.4%; Score 39; DB 3; Local Similarity 100.0%; Pred. No. 6.7e-0 es 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    RRESPONDENCE ADDRESS:
                                REGISTRATION NUMBER: 32,993
                                                                                                                                                                               APPLICATION NUMBER: US/09/291,238
                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                              IP: 07901
                                                                                                                                                                                                                                                                                                                                                                 Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09291238
                                                                                                                                                                                                                                                                                                                                              New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35S Promoter
                                                                                                                                                                                                                                                                                                                                                                                    564 Morrie Avenue
                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
ENTION: DNA Construct Containing Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-09-330-760-5
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                                             US-09-330-760-5
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Matches
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Patent No. 6229075
GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,42
PILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                         TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                     MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                           IMMEDIATE SOURCE:
CLONE: 358 Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 35S Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                   POPOLOGY:
                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                          ENGTH:
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                                                                                                                                                            nucleic acid
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
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                                                                                                                                                                          560 base pairs
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                                                                                                                                 linear
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                                                                                                                   DNA (genomic)
                                                                                                                                                  double
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 49.4%; 1
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DNA Construct
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                                                                                                                                                                                                                                                                                                                                         09/042,426
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; Pred. No
                                                                                                                                                                                                                                                                   135/1
 Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Containing Bacillus
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DB 4; L

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MOLECULE TYPE: DNA (ge

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: 358 Promoter

US-09-328-473-5
Search completed: May 11, 2003, 03:07:42, Job time: 33.6792 secs
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US-09-328-473-5
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                                                                                                                                                Query Match 49.4%; Score 39; DB 4; Length 560; Best Local Similarity 100.0%; Pred. No. 6.7e-06; Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Irvin J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS;
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/328,473
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 360
                                                                         322 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 564 Morris
CITY: Summit
STATE: New Jersey
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                                                                                                             34 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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DNA Construct Containing Bacillus
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1255.289 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Sequence 5, Appli
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appli
Sequence 7, Appli
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Sequence 28, Appli
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Query Match Best Local Matches 7 1 CAT 1 1 CAT 1 CAT	RESULT 1 US-09-963-803 US-09-963-803 US-09-963-803 US-09-963-803 US-09-963-803 US-09-963-803		4 4 5	442	39 40	36 38	ພ ພ ພ ຫ 4 ໜ	320	22222	20 21 22 23
C D	SULT 1 -09-63-803-14 -O9-63-803-14 Sequence 14, Application U Sequence 11, Application U Sequence 11, Application U Sequence 11, Application U Sequence 12, Application V Sequence 12, Application V Sequence 12, Application Chime TITLE OF INVENTION: Chime TITLE OF INVENTION: Chime TITLE OF INVENTION: Viru FILE REFERENCE: 184332042 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 199-0 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 199-0 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-1 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin versio SEQ ID NO 14 LENGTH: 79 TYPE: DNA ORGANISM: Artificial Seq PEATURE: OTHER INFORMATION: Direc OTHER INFORMATION: S7 -09-963-803-14		3 9 9	ωω 9 9	ນ ພູ ພ ຍ ຍ ຍ	3 3 3 9 9 9 9	3 3 3 3 9	ນ ພ ພ ນ ຍ ຍ ຍ ຍ ຍ		39999
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tch 100.0%; Score 79; DB 9; Length 79; al Similarity 100.0%; Pred. No. 2.2e-19; 79; Conservative 0; Mismatches 0; Indels 0; G CATGCTGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTA	963803 1 1cs expression promoters d cassava vein mosaic S/09/963,803 -26 99/03925 IB00/00370 1 1 al desoxynucleotide b	ALIGNMENTS	1 1	US-09-316-622-8 US-09-316-622-6	US-09-316-622-5 US-09-316-622-5 US-09-316-622-5	US-09-316-622-2 US-09-316-622-1 US-10-047-542-101	US-09-810-861B-3 US-09-316-622-3 US-09-316-622-4	US-10-136-221-9 US-10-162-214-9 US-09-758-987-1 US-09-990-659A-15	05-50 60-50 60-50 60-50	ÚS-09-870-375-8 US-09-870-375-9 US-09-870-375-10 US-09-870-375-15 US-09-870-375-15
ngth 79; Indels 0; Gaps 0; ATCTCCACTGACGTA 60 ATCTCCACTGACGTA 60	originating from commelina yellow.		Sequence 7, Appli Sequence 10, Appl	6,0	5,5 2,4,4	5,7,5		sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 15, Appl	e 47, e 33,	Sequence 8, Appli Sequence 9, Appli Sequence 10, Appl Sequence 15, Appl Sequence 6, Appli
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RESULT 2 US-09-963-803-25 ; Sequence 25, Application US/09963803

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LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25
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APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.6%;
Best Local Similarity 93.6%;
Matches 73; Conservative
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
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Best Local
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Publication No.
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CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
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                                                                                                                                                                           NAME/KEY: promoter LOCATION: (1)..(541) OTHER INFORMATION:
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OTHER INFORMATION: promoter MPr1169
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                                                                                            Local Similarity
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Pred. No. 7.5e-16;
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SEQ ID NO 20
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                                                                                                                                                            PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: virus and cassava vein mosaic virus
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PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT 1B00/00370
PRIOR FILING DATE: 2000-10-05
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CURRENT FILING DATE: 2001-09-26
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                 ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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OTHER INFORMATION: promoter MPr1163
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vo. US20030028922A1
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94.7%;
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Pred. No. 9.8e-16;
0; Mismatches 4;
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Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
APPLICANT: Meristern Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
                                                                                                                                                                                                                     RESULT 7
US-09-963-803-21/c
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            Sequence 21, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REPERBYCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: FR 99/03925
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: promoter MPr1165
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                                                                                                                                                                                                                                                                                                                                                                     63
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Local Similarity 94.7%;
nes 72; Conservative
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94.7%;
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Pred. No. 1e-15;
0; Mismatches 4;
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Pred. No. 1.1e-15;
0; Mismatches 4;
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PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 392
TYPE: DNA
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; LOCATION: (1)..(604)
; OTHER INFORMATION:
US-09-963-803-23
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Publication No. US20030028922A1
GEMERAL INFORMATION:
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
TITLE OF INVENTION: Virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
FULL REFERENCE: 184332042
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
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Matches
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 604
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OTHER INFORMATION:
FEATURE:
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ORGANISM: Artificial Sequence
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                                                                        376 TGCCACCTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA 435
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                                                                                               TGCAGACTAGTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGA 65
TGACGCATGCCAC 448
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7 100.0%; Pr
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Pred. No. 1.6e-15;
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Pred. No. 3.7e-15;
0; Mismatches 3;
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RESULT 9

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US-09-870-375-34/c
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Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapuetics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 18433042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOPTWARE: Patentin version 3.1
SEQ ID NOS: 271
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 80
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APPLICANT: MERISTEM THERAPEUTICS

TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CASSETTES,

TITLE OF INVENTION: PLASMIDS, VECTORS, TRANSGENIC PLANTS ET SEEDS INCLUDING

TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME

PILE REFERENCE: PYHMWG1
                                                                                                            Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION; Sequence:Oligodesoxynucleotide
                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                          GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
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                                                                                      Conservative
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                                                                                                            73.4%; Score 58; DB 10; 100.0%; Pred. No. 9.3e-12;
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100.0%; Pred. No. 3.7e-15;
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US-09-870-375-36
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SEQ ID NO 35
LENGTH: 236
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SEQ ID NO 36
LENGTH: 299
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APPLICANT: MERISTEM THERAPEUTICS
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Patent No. US20020083486A1
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Best Local (
                                               Query Match
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CURRENT FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CASSETTES, TITLE OF INVENTION: PLASMIDS, VECTORS, TRANSCENIC PLANTS ET SEEDS INCLUDING TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME FILE REFERENCE: PrHMWG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/870,375
CURRENT FILING DATE: 2001-05-30
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TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CA
TITLE OF INVENTION: PLASMIDS, VECTORS, TRANSCENIC PLANTS ET SEEDS
TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 37
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                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (141)...(195)
OTHER INFORMATION: As2/As2/As1 box
NAME/KEY: misc_feature
LOCATION: (261)
                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:MPr1134
NAME/KBY: enhancer
LOCATION: (20)...(57)
OTHER INFORMATION: Enhancer box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (198)
OTHER INFORMATION: Transcription Initiation Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (78)...(132)
OTHER_INFORMATION: As2/As2/As1 box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:MPr1133
OTHER INFORMATION: promoter
                                                                                                                   OTHER INFORMATION: Transcription Initiation
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                      FEATURE:
  Local Similarity 100 
les 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
73.4%; Score 58; DB 10;
100.0%; Pred. No. 1.5e-11
tive 0; Mismatches 0
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Pred. No.
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                          1.5e-11;
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                                               Length 299
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Patent No. US20020083486A1
GENERAL INFORMATION:
APPLICANT: MERISTEM THERAPEUTICS
APPLICANT: MERISTEM THERAPEUTICS
TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                  Sequence 5, Application US/09870375
Patent No. US20020083486A1
GENERAL INFORMATION:
APPLICANT: MERISTEM THERAPEUTICS
TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PLANTS ET SEEDS INCLUDING
TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME
FILE REFERENCE: PXHMWG1
                                                                                                                        NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 472
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CURRENT APPLICATION NUMBER: US/09/870,375
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 37
SOPTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/870,375
CURRENT FILING DATE: 2001-05-30
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LOCATION: (174].. (228)
OTHER INFORMATION: As2/As2/As1 box
NAME/KEY: TATA signal
LOCATION: (264].. (270)
OTHER INFORMATION: TATA box
NAME/KEY: misc feature
LOCATION: (294)
OTHER INFORMATION: Transcription Initiation Site
                                                                                               TYPE: DNA
OTHER INFORMATION: Description of Artificial Sequence:MPr1130 OTHER INFORMATION: promoter
                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: enhancer
LOCATION: (53)...(90)
OTHER INFORMATION: Enhancer box
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LOCATION: (21)..(28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA
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. 1.5e-11;
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Search completed: May 11, 2003, 06:11:43 Job time : 79.208 secs
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Patent No. US20020083486A1
GENERAL INFORMATION:
                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 28
LENGTH: 80
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Best Local
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CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MERISTEM THERAPEUTICS
TITLE OF INVENTION: SYNTHETIC AND CHIMERIC PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: PLASMIDS, VECTORS, TRANSCENIC PLANTS ET SEEDS INCLUDING
TITLE OF INVENTION: THEM AND PROCESSES FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:Oligodesoxynucleotide
                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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OTHER INFORMATION: Enhancer box
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OTHER INFORMATION: GATA
                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (314)..(368)
OTHER INFORMATION: As2/As2/As1 box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (161)..(168)
OTHER INFORMATION: G-like box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (127)..(133)
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OTHER INFORMATION: Prolamine-like
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                                                                                                            18 ATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 72
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100.0%; Pr
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                                                                                                                                                                  Score 55;
Pred. No.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE SOURCE CONGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 AXO36749 LOCUS DEFINITION ACCESSION VERSION VERSION		C 44 45	42 _.	41	- - w -	37 38	ω u	0 34	ωu	31	30	28	NN	C 25	N N	21	c 20	 	17	16		- -	بر د	a 10		7 0		n) 4.	J N	1	Result No.	
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and Gruber, V. promoters origin sava vein mosaic 15 05-OCT-2000;	34 bp ent WO0058485. 258	ALIGNMENTS	AC025895 AC124997	243	AC090976	AC004600	AC018865 AC107498	AC004259	? !;		AC068026	AC114449	AC115858	AL845366 AC106797	AC119106	AC087220 AC022638	AC115258	35	AC104742	38	2642	AC107106	AC121899	AC022438		AC011264 AC026799	AC010249	AC109962	22	~ N	8 !	ID	SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTCCTCTACTTATCGATCGGTACTGTGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA 01 Jan 5, 2001 this sequence version replaced gi:7767813. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Andereon, S., Baldwin, J., Barna, B., Beda, F., Boguslavkiy, L., Bouts, B., Beda, F., Boguslavkiy, L., Bouts, B., Beda, F., Boguslavkiy, L., Bouts, B., Bouts, B., Boguslavkiy, L., Bouts, B., Compopiano, A., Castie, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Bogue, S., Domino, M., Doyle, M., Collymore, A., College, M., Collymore, A., Cooke, P., Cooke, P., Collymore, A., Cooke, P., Cooke,
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NOTE: This record contains 82 individual
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                                                                        Center project name: L6257
Center clone name: 610_N_12
                                                                                                                                    Contact: sequence submissions@genome.wi.mit.edu
------Project Information
Center project name: L6257
                                                                                                                                                                                                                                                                                                        Center code: WIBR
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larity 100.0%;
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db_xref="taxon:32630"
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Pred. No. 9.1e-05;
Mismatches 0;
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However, will be s
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711 810: gap of 100 bp
811 1530: contig of 720 bp in length
1531 1630: gap of 100 bp
1631 2328: contig of 60°.
                                                                                                                     22800
                                                             24367 24466:
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14 10506: contig of 7
17 10606: gap of .10
17 11318: contig of 7
                                                                                                  23619:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12232: gap of 714 bp 1
12250: contig of 718 bp 1
3050: gap of 100 bp
13772: contig of 722 bp in
1872: gap of 100 hc
14584
                                                         1987: gap of 100 bp 1
22699: contig of 712 bp 1
2799: gap of 100 bp 2
23519: contig of 720 bp 1
3619: gap of 100 bp 24366: contig of 747 bp 1
4466: gap of 100 bp
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12132: c
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14584: contig of 712 bp
684: gap of 100 bp
15399: contig of 715 bp
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21887: contig of 706
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19459: con
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9693: con
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3971: con
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48075 48793; contig of 719 bp in length
48074 48893; gap of 100 bp
48694 49612; contig of 719 bp in length
49613 49712; gap of 100 bp
49713 50414; contig of 702 bp in length
50415 50514; gap of 100 bp
51120; contig of 606 bp in length
51121 51220; gap of 100 bp
51221 51220; gap of 100 bp
51221 51232; contig of 714 bp in length
51935 52034; gap of 100 bp
52035 52034; gap of 100 bp
52036 520375; contig of 714 bp in length
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44714: contig of 733 bp in length
44715 44814: gap of 100 bp
44815 4524: contig of 710 bp in length
45525 45624: gap of 100 bp
46314 46413: gap of 100 bp
46314 46413: gap of 100 bp
46414 47144: contig of 731 bp in length
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47975 48074: gap of 100 bp
47975 480793: contig of 719 bp in length
48074: gap of 100 bp
53560: contig of 709 bp in 53561 53660: gap of 100 bp in 53661 54881: contig of 721 bp in 54482 55194: contig of 713 bp in 55195 55294: gap of 100 bp
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35854 35666; contig of 713 bp in length
36667 36666; gap of 100 bp
36667 37401; contig of 735 bp in length
37402 37501; gap of 100 bp
37502 38204; gap of 100 bp
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39013 3911; contig of 703 bp in length
3912 39311; gap of 100 bp
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30141 30860: contig of 720 bp in length
30861 30960: gap of 100 bp
30961 31694: contig of 734 bp in length
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332615 33313: contig of 699 bp in length
33314 33413: gap of 100 bp
33414 34127: contig of 714 bp in length
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35753: contig of 709
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34127: contig of 714 bp in length
34227: gap of 100 bp
34944: contig of 717 bp in length
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30040: contig of 718
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27595: con
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                                        Rattus norvegicus clone 63 unordered pieces. AC123002
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AC091523.22 GI:18702401
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On Feb 19, 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-APR-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 235505)
Deschamps,S., Dhambliss,
Direct Submission
AC123002.2 GI:21909223
HTG; HTGS_PHASE1.
Rattus norvegicus.
                                                                                    AC123002
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Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
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1 (bases 1 to 235505)
Deschamps,S., Chambliss
Mus musculus Chromosome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/chromosome="1"
/clone="sp3-77a8"
/clone lib="RPCI Mouse BAC Library
50058 c 49581 g 66135 t
                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002 this sequence version replaced gi:16604017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
Submitted (24-JUL-2002) Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 137875)
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Direct Submission
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zny.D.M., Adams,C.,
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.
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COMMENT

Consensus quality: 97350 bases at least Q30 Consensus quality: 101050 bases at least Q20 Consensus Q20

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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                                    Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Katlsson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Liu, M., Louiseged, H., Lozado, R.J., Lu, X., L., Lucier, R., Luna, R., Ma, J., Lucier, R., Luna, R., Ma, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., C., Lewis, L., Massey, E., Mawhiney, B., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neitsens, P., Pattin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, B., Pattin, R., Payton, B., Peery, J., Perez, L., Peters, L., Patkens, R., Primus, B., Pulli, Q., Okwuonu, G., Oragunye, N., Nolsenson, E., Nookenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Stonet, H., Shooshtari, N., Stoother, H., Stonet,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced gi:18860226.
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3 (bases 1 to 178549)
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Direct Submission
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NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 71 contigs. The true order of the pieces
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                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127835 bases at least Q40
Consensus quality: 133351 bases at least Q30
Consensus quality: 138582 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
.----- Project Information
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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2 (bases 1 to 109939)
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The sequence of Homo sapiens Bi
Unpublished
3 (bases 1 to 109939)
Waterston,R.H.
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109939)
10 (bases 1 to 109939)
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (13-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell, Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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6 (bases 1 to 109939)
                                                                                                                                                                         The clone sequenced to the left is RP11-24K2, 200 bp overlap; the clone sequenced to the right is RP11-111G16. Actual start of this clone is at base position 158007 of RP11-24K2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis McPherson additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
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2616. .2722
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20969. 212.
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1604. .2335
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23563. .23584
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24971. .25144
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VERSION
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AC010249
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                                                               -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                  Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7710813.
Center clone name: CIT-HSPC_406F2
            Project Information
Center Project Name: 341206
                                                 Web site: http://www.jgi.doe.gov
                                                                                                                                                       2 (bases 1 to 111081)
DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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38718.
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Pred. No. 1.8e+02;
D; Mismatches 8;
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Summary Statistics
Consensus quality: 104960 bases at least Q40
Consensus quality: 109090 bases at least Q30
Consensus quality: 109623 bases at least Q20
Estimated insert size: 125000; pulse field gel estimation
Betimated insert size: 125000; pulse field gel estimation
Quality coverage: 6.74 in Q20 bases; pulse field gel estimation
Quality coverage: 7.62 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* the finished sequence as it is available and
                                                                                                             N Homo sapiens clone RP11-3K8, LK ACC11264 ACC11264.4 GI:9121012 HTG; HTGS PHASEO.
                                                                                                                                                                                                                                                                                                                                                                            ACTCCTCTACTTATCGATCGGTACTGTGAGACA 34
                                                                                                                                                                                                                                                                                                                                         ACTGCTCCACATATCGATCGGTTCCTAGAAACA 1909
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 137165)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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1 11274: contig of 11274 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                             59.4%;
llarity 75.8%;
Conservative
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/clone_lib="CalTech human BAC library C"
22728 c 24378 g 32141 t 1134 others
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/db_xref="taxon:9606"
/chromosome="5"
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111081: contig of 8238 bp
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102743: contig of 18620 bp in length
102843: gap of unknown length
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36339: contig
36439: gap of
37882: contig
37982: gap of
46574: contig
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13418: contig of 2044 bp in length
13518: gap of unknown length
136339: contig of 22821 bp in length
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Pred. No. 1.8e+02;
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of 14390 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jul 13, 2000 this sequence version replaced gi:6970645. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, clone RP11-3K8
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This record contains 161 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: froject_information
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Center clone name: 3_K_8
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3782:
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10001: contig of 657
10011: gap of 100 b
10795: contig of 694
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3004: gap of 10
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3813: gap of 10
29513: contig of 10
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22518: contig of 6
2618: gap of 10
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117: gap of 100 bp
35721: contig of 704 bp
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137: gap of 100 bp
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Submitted (24-MAR-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                  2 (bases 1 to 162918)
DOE Joint Genome Institute.
                                                                                                                                                                                          1 (bases 1 to 162918)
BOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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132 46731: gap of 100 bp
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127 47526: gap of 100 bp
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43 42042: gap of 100 bp

43 42677: contig of 635 bp

78 42777: gap of 100 bp

78 42777: gap of 100 bp

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55342: gap of 704 bp in length
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44276: contig of 693 bp in length
44376: gap of 100 bp
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                         Earnhart.C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguco, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguco, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kartovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, B., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Moser, M., Neat, D., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwoken, S., Oguh, M., Okwuonu, G., Liede, B., Dace, J., Dace, J., Dace, J., Lozer, J., Dace, J., Lozer, J., Dace, J., Lozer, J., Dace, J., Lozer, J., Lozer, J., Lozer, J., Lozer, J., Dace, J., Lozer, J., Dace, J., Lozer, J., Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cauron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D. Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, I. Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Rarnhayt, R.J., Davis, R.J., Durbin, K.J., Rarnhayt, R.J., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut Creek, CA 94598, USA
On Aug 11, 2001 this sequence version replaced gi:13677048:
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
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DOE Joint Genome Institute and Stanford Human Genome Center.
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ilarity 75.8%;
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norvegicus clone CH230-129C5,
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/db_xref="taxon:9606"
/chromosome="5"
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35261 c 34959 g
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Pred. No. 1
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Payton, B.,
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5, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonnin, D.,
Bryant, N.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20806189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward-Moore, S., Ward-Moore, S., Waren, R., Washington, C., Wallington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 176172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley,K.C.
Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently
consists of 70 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 115261 bases at least Q40
Consensus quality: 121020 bases at least Q30
Consensus quality: 124933 bases at least Q20
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                                                                                                                            Consensus quality: 181059 bases at least Q40
Consensus quality: 183500 bases at least Q30
Consensus quality: 184433 bases at least Q20
Consensus quality: 184433 bases at least Q20
Estimated insert size: 198400; agarcse-fp estimation
Estimated insert size: 198401; sum-of-contigs estimation
Quality coverage: 7.42 in Q20 bases; agarcse-fp estimation
Quality coverage: 7.96 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
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AC022438 4 GI:14579711
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-FBB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 1, 2001 this sequence version replaced gi:7711740.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Project Name: 459338
Center clone name: RPCI-11_137P5
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DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone RP11-137P5, WORKING DRAFT SEQUENCE,
provided by the submittue.

provided by the submittue.

This sequence will be replaced

the finished sequence as soon as it is available and

the accession number will be preserved.

1 71478: contig of 71478 bp in length

71479 71578: gap of unknown length
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Unpublished
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------ Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                         Submitted (19-AUG-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                              3 (bases 1 to 80229)
Shaull,S., Lin,S., Dixon,R.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
                                                                                                                                                                                                                     Submitted (08-AUG-2002) Department Of Chemistry The University Of Oklahoma, 620 Parrington Oval,
                                                                                                                                                                                                                                                        2 (bases 1 to 80229)
Shaull, S., Lin, S., Dixon, R.,
Cook, D., Kim, D. and Roe, B.A.
Direct Submission
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Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L.,
Cook, D., Kim, D. and Roe, B.A.
Medicago truncatula BAC Clone mth1-64n13
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula
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/clone_lib="RPCI human BAC library 11"
39773 c 38649 g 52728 t 800 others
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/db_xref="taxon:9606"
/chromosome="5"
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116162: contig of 22445 bp in length
116262: gap of unknown length
118116: contig of 1854 bp in length
118216: gap of unknown length
137813: contig of 19597 bp in length
137913: gap of unknown length
137915: contig of 1742 bp in length
139755: gap of unknown length
139755: gap of unknown length
17952: contig of 38197 bp in length
178052: gap of unknown length
185791: contig of 7739 bp in length
                                                     2002 this sequence version replaced gi:22218474
                                                                                                                                                            to 80229)
Lin,S., Dixon,R.,
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75.8%;
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80702:
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Pred. No. 1.8e+02;
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mth1-64n13, V
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                                                                                                                                                              May, G., Sumner, L., Gonzales, B.,
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WORKING DRA
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                                                                                                                                                                                                                                                                                                                                                                                          Gonzales, B.,
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SEQUENCE, 28
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                                                                                       208, Norman
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BASE COUNT
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source
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        /clone_lib="Medicago truncatula BAC library H1"
13595 c 12936 g .25254 t 2715 others
                          /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="mth1-64n13"
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80229: contig of 2930
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Query Match

58.8%;

Score 20;

DB 2;

Length 80229;

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REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
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                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 0%
Sequencing vector: plasmid; 10%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 157599 bases at least Q40
Consensus quality: 158199 bases at least Q30
Consensus quality: 158386 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 159446; sum-of-contigs
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AC121899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: M_BB0166J12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 159746)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 16.21 in Q20 bases; agarose-fp Quality coverage: 12.58 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 159746)
McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                 8022
8122
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                  organism="Mus musculus"
                                                                 Location
db_xref="taxon:10090"
                                                                                  8021: contig of 8021 bp in length
8121: gap of unknown length
26511: contig of 18390 bp in length
26611: gap of unknown length
76565: contig of 49954 bp in length
76665: gap of unknown length
76665: gap of unknown length
159746: contig of 83081 bp in length.
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Delamey, K. R., Delgado, O., Demn, A. L., Ding, Y., Dinh, H. H.,
Douthwaite, K. J., Delgado, O., Demn, A. L., Ding, Y., Dinh, H. H.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edgar, M., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Holloway, C., Hollins, B.,
Homei, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.,
Li, J., Li, Charage, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, C., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Li, J., Li, Z., Lichtarge, O., Martinez, E.,
Maseey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E.,
Maseey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E.,
Neuten, M., Okwonu, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Scherer, S., Scott, G., Shen, H., Stone, H.,
Sutton, A., State, M., State, H., Stone, H.,
Sutton, A., State, M., State,
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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Mammalia; Eutheria;
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 170083)
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                                                                                                                                                                                                                                                                                                                          On Jul 13, 2002 this sequence version replaced gi:18701531
                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNIF
                                                                                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
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NOTE: Estimated insert size may differ from sequence length
[see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h
NOTE: This is a "working draft" sequence. It currently
consists of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. gap of contig contig of 1039 bp in l unknown length in length data.html).

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                                                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 222667 bases at least Q40
Consensus quality: 223874 bases at least Q30
Consensus quality: 224621 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 226459; sum-of-contigs
Quality coverage: 17.88 in Q20 bases; agarose-fp
Quality coverage: 11.92 in Q20 bases; sum-of-contig
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SEQUENCE, 13
AC129318
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 227789)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (28-UTL-2002) Genome Sequencing Center, 4444 Forest
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                       Center project name: M_BA0464B17
                                                                                                                                                                                                                                                                                                                                                                   Contact: submissions@watson.wustl.edu
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McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clor
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* be preserved.
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Similarity 82.1%;
23; Conservative
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                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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FEATURES
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Matches 23; Conservative
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

	JOURNAL	TITLE	REFERENCE AUTHORS		SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 BH746858 LOCUS DEFINITION
Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of	Arabidopsis Genome Unpublished (2001) Contact: Joseph R. Ecker	,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the	1 (bases 1 to 224) Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	thale cress. Arabidopsis thaliana	<pre>sequence. BH746858 BH746858.1 GI:18959973 GSS.</pre>	BH746858 224 bp. DNA linear GSS 27-FEB-2002 SALK 003694.51.40.x Arabidopsis thaliana TDNA insertion lines Arabīdopsis thaliana genomic clone SALK_003694.51.40.x, DNA

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RESULT 2
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A Sequence-Indexed Library of Insertion Mutations in the
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the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
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39; Conservative
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A Sequence-Indexed Library of Insertion Mutations in the
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Unpublished (2001)
Contact: Joseph R. Ecker
                                    Alonso,J.M., Leisse,T.J., Barajas,P.,
C., Jeske,A., Karnes,M., Kim,C.J., P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Inserti
                                                                                                                                                                                                                                                                                                                     #H747013 153 bp SALK 008070.43.05.x Arabidopsis Arabidopsis thaliana genomic clo
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                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 153)
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Pax: 858 558 6379
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 34 c 36 g 47 t
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                             Ecker,J.R.
Library of Insertion Mutations in the
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Parker,H.,
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Prednis, L., Shinn, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Salk Institute Genomic Stalk Institute for Biological Studies
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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Unpublished (2001)
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C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predni
Zimmerman,J. and Ecker,J.R.
Sequence-Indexed Library of Insertion Mutations in
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 37 c 33 g 36 t
                 /strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
clone_lib="Arabidopsis thaliana TDNA insertion lines"
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165 bp DNA linear GSS 27-FEB-2002 SALK 016522.55.50.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_016522.55.50.x, DNA
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Unpublished (2001)
Contact: Joseph R. Ecker
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A Sequence-Indexed Library of Insertion Mutations in the
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39; Conservative 0; Mismatches 0;
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/notes"PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 43 c 39 g 38 t
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/db_xref="taxon:3702"
/clone="SALK_016522.55.50.x"
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Prednis, L., Shinn,
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BH802465/c
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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1008026E10.y2 1008 -
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Unpublished (2001)
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                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 177)
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C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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                      1 (bases 1 to Walbot, V.
                                                                                                                          Zea mays
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                                                                                                                                           Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAIK_045268.54.50.x"
/clone="SAIK_PA5268.54.50.x"
/clone="PCR_was performed on Arabidopsis thaliana lines"
/note="PCR_was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.saik.edu/tdna_protocols.html"
54 a 43 c 40 g 38 t
genomic sequences found using engineered RescueMu transposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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1 (bases 1 to 190)
1 (bases 7 to 190)
1 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Godrinab
                                                               Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies
                                                                                                      Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University
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Zimmerman, J. and Ecker, J.R.
Sequence-Indexed Library of Insertion Mutations in the
0 N. Torrey Pines Road, La Jolla,
858 453 4100 x1752
858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
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/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
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db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                  10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predni
, Ziamerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                           Class: TDNA tagged
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61
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                                                                                                                                                                                                                                                                                                                                                                               ecker@salk.edu
                directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used ca
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                               /clone="SALK_045097.54.25.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://sigmal.salk.edu/tdna_protocols.html"
a 52 c 41 g 45 t
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/clone="SALK_019366.54.25.x"
                                                                                                                                                                                                                     strain="Columbia
                                                                                                                                                                                                                                          organism="Arabidopsis thaliana'
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Pred. No.
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RESULT 13
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                Local Similarity
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             BH753813 215 bp DNA linear GSS SALK 029677.55.00.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 029677.55.00.x,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis Genome 
Unpublished (2001)
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A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                     /db xref="taxon:3702"
/clone="SALK 03534.55.75.x"
/clone="SALK 03534.55.75.x"
/clone="SALK 03534.55.75.x"
/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
a 56 c 52 g 48 t
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/strain="Columbia 0"
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Pred. No.
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Institute Genomic Analysis Laboratory (SIGnAL)
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105 GATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USP
                         Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pax: 858 558 6379
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,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,
, Zimmerman,J. and Ecker,J.R.
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                                                                               C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Predni
Zimmerman, J. and Ecker, J.R.
Sequence-Indexed Library of Insertion Mutations in
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/db xref="taxon:3702"
/db xref="taxon:3702"
/clone="BALK 029677.55.00.x"
/clone=lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 56 c 50 g 46 t
Joseph R. Ecker
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Pred. No.
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Kim, C.J., Parker, H.,
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0.0042;
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Prednis, L., Shinn, I
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Prednis, L., Shinn, 1
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                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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220 bp DNA LINGAL TOO INC. SALK 017469.51.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_017469.51.60.x, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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                                                                                                                                                                                                                 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Genome 
Unpublished (2001)
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                                                                                                                                                                                                                                                                                      ecker@salk.edu
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/strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK_017469.51.60.x"
/clone="SALK_017469.51.60.x"
/clone="FAReabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
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/clone="SALK 033710.53.75.x"
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                                                                                                                                     organism="Arabidopsis thaliana"
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100.0%; Pr/
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Prednis, L., Shinn,
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> BASE COUNT 67 a elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" a 55 c 48 g 50 t

Matches Best Local Query Match 39; Similarity Conservative 100.0%; 49.48; 0 Score 39; DB 17; Pred. No. 0.0043; Mismatches 0 Length 220; Indels 0 Gaps

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ORIGIN

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